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OM protein - protein search, using sw model

Run on: October 4, 2004, 12:49:31 ; Search time 324 Seconds
(without alignments)

414.167 Million cell updates/sec

Title: US-09-807-148-2

Perfect score: 2282
Sequence: 1 MLLSVPLLLGLLGLAVAEPA.....EEDKEDEEDVPQAKDEL 417

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1351062 seqs, 32179191 residues

Total number of hits satisfying chosen parameters: 1351062

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2282	100.0	417	10	US-09-807-148-2
2	2282	100.0	417	14	US-10-161-959-29
3	2282	100.0	417	15	US-10-367-093-14
4	2278	99.8	416	15	US-09-828-000-2
5	2278	99.8	416	15	US-10-405-588-2
6	2163.5	94.8	416	14	US-10-316-253-2
7	2163.5	94.8	416	14	US-10-316-253-4
8	2163.5	94.8	416	14	US-10-316-253-6
9	1408.5	61.7	395	15	US-10-369-493-6343
10	1216	53.3	435	12	US-10-425-114-70304
11	1213	53.2	421	16	US-10-767-701-46544
12	1206	52.8	442	12	US-10-425-114-46869
13	1198	52.5	424	16	US-10-437-963-20420
14	1192	52.2	431	16	US-10-767-701-44015
15	1176.5	51.6	420	9	US-09-844-006A-2

ALIGNMENTS

RESULT 1

US-09-906-393A-36
; Sequence 36, Application US/09906393A
; Publication No. US20030039970A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Zhou
; APPLICANT: Xiao, Wuhan
; TITLE OF INVENTION: METHOD OF PROGNOSING CANCER AND THE PROTEINS INVOLVED
; FILE REFERENCE: 1720-1-001CIP
; CURRENT APPLICATION NUMBER: US/09/906,393A
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/218,761
; PRIOR FILING DATE: 2000-07-17
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 36
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-906-393A-36

Query Match 100.0%; Score 2282; DB 10; Length 417;
Best Local Similarity 100.0%; Pred. No. 7.5e-163;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLSVPLLLGLLGLAVAEPAVYFKQFLDGGTWSWIESKHKSDFGKVLSSGKFGYGE 60
DB 1 MLLSVPLLLGLLGLAVAEPAVYFKQFLDGGTWSWIESKHKSDFGKVLSSGKFGYGE 60
QY 61 EKDKGLQTSQDARFYALSASPEPPFNKQTLVQVTVKHEQNDCCGGYVKLPFNSLDQT 120
DB 61 EKDKGLQTSQDARFYALSASPEPPFNKQTLVQVTVKHEQNDCCGGYVKLPFNSLDQT 120
QY 121 DMHGDSEYNIIMPGPICGPTKKVHVIYNYKGNVLINKDRCKDDETHLYTLVRDN 180
DB 121 DMHGDSEYNIIMPGPICGPTKKVHVIYNYKGNVLINKDRCKDDETHLYTLVRDN 180
QY 181 TVEVKIDNSQVBSGSLEDDWDFLPKKTKDPASKPEDWDERAKIDDDTDSKPEDWDKXPE 240

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Sequence 45264, A
Sequence 153808,
Sequence 46, Appl
Sequence 57598, A
Sequence 3, Appl
Sequence 3, Appl
Sequence 44621, A
Sequence 54997, A
Sequence 38848, A
Sequence 129, App
Sequence 1095, App
Sequence 44768, A
Sequence 39041, A
Sequence 68, Appl
Sequence 190356,
Sequence 3546, App

US-10-424-599-190958
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Db 301 PDPSIYAYDNFVGLDLMQVKSFTIDNPLIINDAYAEFGNETGWYTKAAEQMKDK 360
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RESULT 2
US-10-161-959-29
; Sequence 29, Application US/10161959
; Publication No. US20030096748A1
; GENERAL INFORMATION:
; APPLICANT: Holoshitz, Joseph
; APPLICANT: Ling, Song
; TITLE OF INVENTION: Methods and Compositions for the Treatment of Diseases Associated
; FILE REFERENCE: UM-07135
; CURRENT APPLICATION NUMBER: US/10/161,959
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: 60/295,691
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-161-959-29

Query Match 100.0%; Score 2282; DB 14; Length 417;
Best Local Similarity 100.0%; Pred. No. 7.5e-163;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLSVPLLLGLLGLAFAEPVYKQFPLDGDGWTSRWIESKHKSDFGKFLVSSGKPYGDE 60
Db 1 MLLSVPLLLGLLGLAFAEPVYKQFPLDGDGWTSRWIESKHKSDFGKFLVSSGKPYGDE 60
Qy 61 EKDKGLQTSODARFYALSASFEPFNKQTLVVQFTVKHEQNDICGGYVVKLFPNSLDQT 120
Db 61 EKDKGLQTSODARFYALSASFEPFNKQTLVVQFTVKHEQNDICGGYVVKLFPNSLDQT 120
Qy 121 DMHGDSEYNIMFGPDICGPTKKVHVFYNYKGNVLINKDIRCKDDEFTHLTYLIVRPN 180
Db 121 DMHGDSEYNIMFGPDICGPTKKVHVFYNYKGNVLINKDIRCKDDEFTHLTYLIVRPN 180
Qy 181 TYEVKIDNSQVSGSLEDDWDFLPKKIKDPDASKPEDWDERAKIDPTDTSKPEDWPKPE 240
Db 181 TYEVKIDNSQVSGSLEDDWDFLPKKIKDPDASKPEDWDERAKIDPTDTSKPEDWPKPE 240
Qy 241 HIPDPDAKPEDWDEMDGWEPPVIONPEYKGEWKPRQIDNPDKYKGTWIHPEIDNPEYS 300
Db 241 HIPDPDAKPEDWDEMDGWEPPVIONPEYKGEWKPRQIDNPDKYKGTWIHPEIDNPEYS 300
Qy 301 PDPSIYAYDNFVGLDLMQVKSFTIDNPLIINDAYAEFGNETGWYTKAAEQMKDK 360
Db 301 PDPSIYAYDNFVGLDLMQVKSFTIDNPLIINDAYAEFGNETGWYTKAAEQMKDK 360
Qy 361 QDEEQLKEEEDKKKEEAEADKEDDEKDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 417
Db 361 QDEEQLKEEEDKKKEEAEADKEDDEKDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 417
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RESULT 3
US-10-367-093-14
; Sequence 14, Application US/10367093
; Publication No. US20030216315A1
; GENERAL INFORMATION:
; APPLICANT: Duke University
; APPLICANT: Nicchitta, Chris
; APPLICANT: Baker-LePain, Julie
; TITLE OF INVENTION: MODULATION OF IMMUNE RESPONSE BY NON-PEPTIDE BINDING STRESS RESPO
; FILE REFERENCE: 160/145
; CURRENT APPLICATION NUMBER: US/10/367,093
; CURRENT FILING DATE: 2003-02-13
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-367-093-14

Query Match 100.0%; Score 2282; DB 15; Length 417;
Best Local Similarity 100.0%; Pred. No. 7.5e-163;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLSVPLLLGLLGLAFAEPVYKQFPLDGDGWTSRWIESKHKSDFGKFLVSSGKPYGDE 60
Db 1 MLLSVPLLLGLLGLAFAEPVYKQFPLDGDGWTSRWIESKHKSDFGKFLVSSGKPYGDE 60
Qy 61 EKDKGLQTSODARFYALSASFEPFNKQTLVVQFTVKHEQNDICGGYVVKLFPNSLDQT 120
Db 61 EKDKGLQTSODARFYALSASFEPFNKQTLVVQFTVKHEQNDICGGYVVKLFPNSLDQT 120
Qy 121 DMHGDSEYNIMFGPDICGPTKKVHVFYNYKGNVLINKDIRCKDDEFTHLTYLIVRPN 180
Db 121 DMHGDSEYNIMFGPDICGPTKKVHVFYNYKGNVLINKDIRCKDDEFTHLTYLIVRPN 180
Qy 181 TYEVKIDNSQVSGSLEDDWDFLPKKIKDPDASKPEDWDERAKIDPTDTSKPEDWPKPE 240
Db 181 TYEVKIDNSQVSGSLEDDWDFLPKKIKDPDASKPEDWDERAKIDPTDTSKPEDWPKPE 240
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Db 241 HIPDPDAKPEDWDEMDGWEPPVIONPEYKGEWKPRQIDNPDKYKGTWIHPEIDNPEYS 300
Qy 301 PDPSIYAYDNFVGLDLMQVKSFTIDNPLIINDAYAEFGNETGWYTKAAEQMKDK 360
Db 301 PDPSIYAYDNFVGLDLMQVKSFTIDNPLIINDAYAEFGNETGWYTKAAEQMKDK 360
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Db 361 QDEEQLKEEEDKKKEEAEADKEDDEKDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 417

RESULT 4
US-09-828-000-2
; Sequence 2, Application US/09828000
; Publication No. US20030078198A1
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/09/828,000
; CURRENT FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Calreticulin
US-09-828-000-2

Query Match 99.8%; Score 2278; DB 10; Length 416;
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Db 182 DGSQAQTGSLEEDWDLPPAKIKDPDASKPEDWDEREYIDDAEDAKPEDWEXPEHIPPDP 241
QY 247 AKKPEDWDEMDGWEPPVIONPEYKGEWKPRQIDNPDKYGTWVHPEINPNPSPDPSIY 306
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QY 307 AYDNFVGLDLWQVKSGLTFDNFLITNDAYAEFCNETGWYTKAAEKQMKDKQDEROR 356
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QY 367 LKEEEDKKRKEEEDKEDDDDKDEDEDE 399
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RESULT 10
US-10-425-114-70304
; Sequence 70304, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 70304
; LENGTH: 435
; TYPE: PRT
; ORGANISM: Zea mays subsp. mexicana
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMROTEOSINT102C08_FLI.pep
US-10-425-114-70304

Query Match 53.3%; Score 1216; DB 12; Length 435;
Best Local Similarity 53.8%; Pred. No. 6,3e-83;
Matches 228; Conservative 69; Mismatches 105; Indels 22; Gaps 8;

QY 4 SVPLLLGLGLVAEPAYVFKQFLDGGWTSRWIESKHKSD---FGKVLSSGKFGYDE 60
Db 24 AVAALLALASVAAGVFFQEF--EDGWESRWVSKWKDENMAGENNHTSGKXNGDA 81
QY 61 EKDGLQTSQARFYALSASPEPSNKGOTLVQFTVKHEQNDICGGYVKKLPFNSLDQT 120
Db 82 E-DKGIQTSDFRYFVIAEYFESFNKDKTLVLFQSVKHEQKLDCCGGYVKKLGGVDQK 140
QY 121 DMHGDSEYNMFGPDICGPGTKKVHVIFNYKGNVLINKDKODFTHLYTLIVRPDN 180
Db 141 KEGDTSYINFGPDICGYSYTKVHTILTQDGNHLLKDVPCETDQLTHTVTLIRPDA 200
QY 181 TYEVKIDNSQVSGSLEDWDFLPPKKIKDPDASKPEDWDERAKIDDDPTDSKPEDWDX-P 239
Db 201 TYSILIDNEEKQTSIYEHWDILPPKKIKDPDASKPEDWDXKEYIPDPDKKPEGYDDIP 260
QY 240 EHIPDPDAKPEDWDEMDGWEPPVIONPEYKGEWKPRQIDNPDKYGTWVHPEINPNPEY 299
Db 261 KEIPDPDAKPEDWDEMDGWEPPVIONPEYKGEWKPRQIDNPDKYGTWVHPEINPNPEY 320
QY 300 SPDPISIYDNFVGLDLWQVKSGLTFDNFLITNDAYAEFCNETGWYTKAAEKQMKDK 359
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QY 414 KDEL 417
Db 432 HDEL 435

RESULT 11
US-10-767-701-46544
; Sequence 46544, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 46544
; LENGTH: 421
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C5075_1.pep
US-10-767-701-46544

Query Match 53.2%; Score 1213; DB 16; Length 421;
Best Local Similarity 54.0%; Pred. No. 1e-82;
Matches 227; Conservative 69; Mismatches 110; Indels 14; Gaps 7;

QY 4 SVPLLLGLGLVAEPAYVFKQFLDGGWTSRWIESKHKSD---FGKVLSSGKFGYDE 60
Db 10 AVAALLALASVAAGVFFQEF--EDGWESRWVSKWKDENMAGENNHTSGKXNGDA 67
QY 61 EKDGLQTSQARFYALSASPEPSNKGOTLVQFTVKHEQNDICGGYVKKLPFNSLDQT 120
Db 69 E-DKGIQTSDFRYFVIAEYFESFNKDKTLVLFQSVKHEQKLDCCGGYVKKLGGVDQK 126
QY 121 DMHGDSEYNMFGPDICGPGTKKVHVIFNYKGNVLINKDKODFTHLYTLIVRPDN 180
Db 127 KEGDTPYSIMFGPDICGYSYTKVHTILTQDGNHLLKDVPCETDQLTHTVTLIRPDA 186
QY 181 TYEVKIDNSQVSGSLEDWDFLPPKKIKDPDASKPEDWDERAKIDDDPTDSKPEDWDX-P 239
Db 187 TYSILIDNEEKQTSIYEHWDILPPKKIKDPDASKPEDWDXKEYIPDPDKKPEGYDDIP 246
QY 240 EHIPDPDAKPEDWDEMDGWEPPVIONPEYKGEWKPRQIDNPDKYGTWVHPEINPNPEY 299
Db 247 KEIPDPDAKPEDWDEMDGWEPPVIONPEYKGEWKPRQIDNPDKYGTWVHPEINPNPEY 306
QY 300 SPDPISIYDNFVGLDLWQVKSGLTFDNFLITNDAYAEFCNETGWYTKAAEKQMKDK 359
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QY 360 KODEEQRKKEEEDKKR---KKEEBAEDKEDDEDEKDEED---BEDKBEDEEDVPGQA 417
Db 367 EAEK-----KKEEEDAAGGDEDDLEDEDEDEKADEKADSD---AEDSKDSDDEKHEDEL 421

RESULT 12
US-10-425-114-46869
; Sequence 46869, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
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; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 46869
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLB73073A05_FLI.pep
US-10-425-114-46869

Query Match 52.8%; Score 1206; DB 12; Length 442;
Best Local Similarity 53.2%; Pred. No. 3.6e-82;
Matches 223; Conservative 72; Mismatches 112; Indels 12; Gaps 6;

QY 4 SVPLLLGLGLAFAEPAVYFKEQFLDGDGWTSEWIESKHSD---FGKFLVSSGKFYGD 60
DB 31 AVAALLALASVAAGVFFQKFP--EDGWESRWKSEWKKDENMAGENHTSGKWN 88
QY 61 EKDGLQTSODARFALSASFEPPSNKGOTLVQFTVKHEQNDICGGGVYKLP-PNSLDO 119
DB 89 E-DKGIQTSDEYRFYALSAEYFPEFSNKGOTLVQFSVKHEQKLDICGGGVYKLG 147
QY 120 TMHGDSEYNIMFGPDICGPGTKKVVHVI FNYKGNVLINKDIRCKDDEFTHTLYLIVRPD 179
DB 148 KFGGDTSYIMFGPDICGPGTKKVVHVI FNYKGNVLINKDIRCKDDEFTHTLYLIVRPD 207
QY 180 NTEVIDNSQVSGSLEDWDFLPKKIKDPDASKPEDWDERAKIDPTDSKPEDW 238
DB 208 ATYSILIDNEKQTSYIEHWDILPPKKIKDPDASKPEDWDERAKIDPTDSKPEDW 238
QY 239 PEHIPDDAKKPEDWDEEMDGEWEPVIONPEYKGEWKPQIDNPDKYKGTWHPIDNPE 298
DB 268 KPEIPDDAKKPEDWDEEDGWTAPTIPNPEYKGPWKQKKIKNPYQGWKAPMIDNPD 327
QY 299 YSDPSIYAYDNFVGLDLWQVSGTIFDNFLINDEAYAEFGNETGWVTKAAEKOMK 358
DB 328 FKDDPIYAFDSLKYIGIELWQVSGTIFDNFLINDEAYAEFGNETGWVTKAAEKAA 387
QY 359 DKDEORLKEEEDKKRKEEAEDEKDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 417
DB 388 DEAEK-----KXBEEDAAGKGGDEDDDEDEDEDEDEDEDEDEDEDEDEDEDEDE 442

RESULT 13
US-10-437-963-201420
; Sequence 201420, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 201420
; LENGTH: 424
; -TYPE: PRT
; ORGANISM: Oryza sativa

; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_96798C.1.pep
US-10-437-963-201420

Query Match 52.5%; Score 1198; DB 16; Length 424;
Best Local Similarity 53.1%; Pred. No. 1.4e-81;
Matches 221; Conservative 69; Mismatches 108; Indels 18; Gaps 5;

QY 4 SVPLLLGLGLAFAEPAVYFKEQFLDGDGWTSEWIESKHSD---FGKFLVSSGKFYGD 60
DB 14 AVAALLALASVAAGVFFQKFP--EDGWESRWKSEWKKDENMAGENHTSGKWN 71
QY 61 EKDGLQTSODARFALSASFEPPSNKGOTLVQFTVKHEQNDICGGGVYKLP-PNSLDO 120
DB 72 E-DKGIQTSDEYRFYALSAEYFPEFSNKGOTLVQFSVKHEQKLDICGGGVYKLG 130
QY 121 DMHGDSEYNIMFGPDICGPGTKKVVHVI FNYKGNVLINKDIRCKDDEFTHTLYLIVRPD 180
DB 131 KFGGDTSYIMFGPDICGPGTKKVVHVI FNYKGNVLINKDIRCKDDEFTHTLYLIVRPD 190
QY 181 TYEYKIDNSQVSGSLEDWDFLPKKIKDPDASKPEDWDERAKIDPTDSKPEDW 239
DB 191 TYTILIDNVEKQSGSIYEHWDILPPKKIKDPDASKPEDWDERAKIDPTDSKPEDW 250
QY 240 EHIPDDAKKPEDWDEEMDGEWEPVIONPEYKGEWKPQIDNPDKYKGTWHPIDNPE 299
DB 251 KEIPDDAKKPEDWDEEDGWTAPTIPNPEYKGPWKQKKIKNPYQGWKAPMIDNPD 310
QY 300 SPDSIYAYDNFVGLDLWQVSGTIFDNFLINDEAYAEFGNETGWVTKAAEKOMK 359
DB 311 KDDPIYAFDSLKYIGIELWQVSGTIFDNFLINDEAYAEFGNETGWVTKAAEKAA 370
QY 360 KDDEORLKEEEDKKRKEEAEDEKDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 415
DB 371 -----EAEKKKEEAEKAGEDDDDDDEDEDEDEDEDEDEDEDEDEDEDEDE 415

RESULT 14
US-10-767-701-44015
; Sequence 44015, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 44015
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(431)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C10317_1.pep
US-10-767-701-44015

Query Match 52.2%; Score 1192; DB 16; Length 431;
Best Local Similarity 53.1%; Pred. No. 3.9e-81;
Matches 229; Conservative 62; Mismatches 110; Indels 30; Gaps 8;

QY 3 LSVPLLLGLGLAFAEPAVYFKEQFLDGDGWTSEWIESKHSD---FGKFLVSSGKFYGD 59
DB 15 VAAALIALASVAGVFFQKFP--DDGWEDRWKSDWKDDNTAGWENHTSGKWN 72
QY 60 EKDGLQTSODARFALSASFEPPSNKGOTLVQFTVKHEQNDICGGGVYKLP-PNSLDO 119

73	AD-DXGIGTSEDYRFAISAQYPEFSNKDKTILVLQFSVRHEQKLDCCGGYVLKLLGSDVDQ	131
120	TMHGDSYNIIMPFGDTCGGPTKKVHVIFNYKGNVLINKDIRCKDDETHYTLIIVRPD	179
132	KKFGDGTYSIMFGPDICGYATKKVHAILTNGKNHLIKKELPGETDQLTHYTLIIRPD	191
180	NTYEVKINISQVSGSLIEDWCFLPPKKIKDPAKSPEDWDERAKTDDPTDSKPEDWK-	238
192	ATYSILIDNEKSGSIVDWDILPPKKIKDPAKSPEDWDDKEYIPDEDKKPEGYDDI	251
239	PEHIDPPAKKPEDWDEMDGENEPPVIONPEYKGEWKPRQIDNPYKGTWTHPIIDNPE	298
252	PKXEIDPPAKKPEDWDEEDGEWTAPTIPIPEYKGPWKQKIKNPDKGKWKAPIDINDP	311
299	YSFDESIYAYDNFVGLGLDLQVKSGTIFNFILITNDEAYAEFNGETWGTAKAEQMKQ	358
312	PKDDPYIVAFDSLKHIGIELQVKSGLTFDNIILITDPEYAKKLAIVETWKGQKDAEKA	371
359	DQDDEEQLKBEEDKKKEK-----PEAKDKDEE--DKDEDEEDED-----KEEDE	406
372	D-----EAEKRLBECFSLXSASAKDDDLVDVEDEDEDADDKDKADHSDTBEA	420
407	EDVPGQAKDEL	417
421	EDSEAKHDEL	431

RESULT 15

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US-09-844-006A-2
; Sequence 2, Application US/09844006A
; Patent No. US20020083496A1
; GENERAL INFORMATION:
; APPLICANT: Wyatt, Sarah
; APPLICANT: Tsou, Pei-Lan
; APPLICANT: Robertson, Dominique
; APPLICANT: Boss, Wendy
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH INCREASES IN CALCIUM STORES
; FILE REFERENCE: 5051.503
; CURRENT APPLICATION NUMBER: US/09/844, 006A
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 60/200,233
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Zea mays
US-09-844-006A-2

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Query Match	51.6%	Score 1176.5	DB 9	Length 420
Best Local Similarity	51.9%	Pred. No. 5.5e-80		
Matches 217	Conservative	74	Mismatches 116	Indels 11
Gaps	5			
QY	4	SVPLLGLLGLAAVPAVYFKQDFLDGDTGNTSRWIESKHKSD---FGKFFVLSGSKFYGYDE	60	
DB	10	AVAALLALASVAAVAGEVFQKFX-EDGWESRWKSEWKDENMAGEMNHTSKWNGDA	67	
QY	61	EKKGLGLOTSODARFYALASAFEPSPNKGOTLVQVFTVYKHEQNDICGGGYVYKLPENSIDQT	120	
DB	68	E-DKGITQSDYFYAISAFYEPSPNKKDLVLQFQSVYKHEQKLDICGGGYVYKLPJGGDVDDQK	126	
QY	121	DMAGDSEYNIMFGPDI CGPGTKKHVHIFNYKGNVLINKDIRCKDDBFTHLYTLVLVAPDN	180	
DB	127	TLGDTSYSIISRPDI SRYSKTKVHTLTLDKGNHLIKDVPQCTDQLTHVYTFIIRPDA	186	
QY	181	TYEVKIDNSQVESGSLEDDWFLPPKKIKQDASKPDPDWERAKIDIDPTTSKEDWDK-P	239	
DB	187	TYSLIIDNEKHTGSIYEHWDILPPKKIKQDPAKKPEDWDCKEYIPEDKKPEGYDDIP	246	
QY	240	EHIPDPDAKKPDWDEEMDGEWEPVQINPEYKGEWKPQIDNPDYKGTWIHPEDINPEY	299	
DB	247	KEIPDPDAKKPDWDDSEDEWTAFTIPNEYKGPWKOKKIKPNYQGWKAKMIDNPDE	306	

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OM protein - protein search, using sw model

Run on: October 4, 2004, 12:49:26 ; Search time 23 Seconds
(without alignments)
936.001 Million cell updates/sec

Title: US-09-807-148-2
Perfect score: 2282
Sequence: 1 MLLSVPELLGLGLAVAEPA.....EDKKEDEEDVPGQAKDEL 417

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2278	99.8	416	4	US-09-828-000-2
2	1224.5	53.7	415	3	US-08-675-816-2
3	971	42.6	180	4	US-09-828-000-3
4	799	35.0	593	1	US-08-296-362-2
5	731.5	32.1	610	4	US-09-976-594-947
6	641.5	28.1	542	3	US-08-675-816-6
7	340	14.9	61	4	US-09-828-000-4
8	327	14.3	61	4	US-09-828-000-8
9	189	8.3	35	4	US-09-828-000-7
10	184.5	8.1	714	2	US-08-990-114-3
11	184.5	8.1	714	4	US-09-241-333-3
12	184.5	8.1	740	1	US-08-257-073-5
13	175.5	7.7	1162	2	US-08-728-323A-2
14	175.5	7.7	1162	4	US-09-298-568-2
15	175.5	7.7	1162	4	US-09-410-399-2
16	163	7.1	905	2	US-08-574-959A-9
17	163	7.1	905	3	US-09-357-014-9
18	163	7.1	1135	3	US-08-574-959A-7
19	163	7.1	1135	3	US-09-357-014-7
20	154	6.7	1312	4	US-09-345-882-29
21	151	6.6	27	4	US-09-828-000-5
22	151	6.6	740	3	US-09-022-983-5
23	150.5	6.5	546	3	US-08-935-855-20
24	149	6.5	411	2	US-08-741-134-6
25	146	6.4	754	3	US-09-214-564A-2
26	146	6.4	764	4	US-09-370-838-67
27	143.5	6.3	197	4	US-09-486-147-40

28	143.5	6.3	240	2	US-08-114-555A-8	Sequence 8, Appli
29	143.5	6.3	240	3	US-08-559-397A-14	Sequence 14, Appli
30	137	6.0	633	1	US-08-458-477A-5	Sequence 5, Appli
31	137	6.0	633	2	US-09-033-153-5	Sequence 5, Appli
32	137	6.0	633	3	US-09-325-430B-5	Sequence 2, Appli
33	137	6.0	765	2	US-08-663-112-2	Sequence 7, Appli
34	137	6.0	1166	4	US-09-200-650E-7	Sequence 26, Appli
35	137	6.0	3052	2	US-08-557-122A-26	Sequence 26, Appli
36	137	6.0	3052	4	US-08-282-666-26	Sequence 5, Appli
37	135	5.9	295	2	US-08-679-785-5	Sequence 5, Appli
38	135	5.9	295	3	US-09-196-525-5	Sequence 5, Appli
39	135	5.9	295	3	US-09-318-317-5	Sequence 22, Appli
40	135	5.9	295	4	US-09-177-165A-22	Sequence 194, App
41	134.5	5.9	231	3	US-09-461-697-194	Sequence 192, App
42	134.5	5.9	232	3	US-09-461-697-192	Sequence 190, App
43	134.5	5.9	238	3	US-08-461-697-190	Sequence 188, App
44	134.5	5.9	257	3	US-09-461-697-188	Sequence 186, App
45	134.5	5.9	272	3	US-09-461-697-186	

ALIGNMENTS

RESULT 1

US-09-828-000-2
; Sequence 2, Application US/09828000
; Patent No. 6596690
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/09/828,000
; CURRENT FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Calreticulin
US-09-828-000-2

Query Match 99.8%; Score 2278; DB 4; Length 416;
Best Local Similarity 100.0%; Pred. No. 5.6e-199;
Matches 416; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLLSVPELLGLGLAVAEPAVYFKQFLDGDGWTSEKHSDFGKPVLSGKFYGD	60
Db	1	MLLSVPELLGLGLAVAEPAVYFKQFLDGDGWTSEKHSDFGKPVLSGKFYGD	60
Qy	61	EKDKGLOTSDARFVALSASFEPPFNKGOTLVVQFTVXHEQNDGCGGVYKLPFNSLDT	120
Db	61	EKDKGLOTSDARFVALSASFEPPFNKGOTLVVQFTVXHEQNDGCGGVYKLPFNSLDT	120
Qy	121	DMHGDSEYIMFGPDICGPGTKKHVIFNYKGNVLINKDIRCKDDEFTHLYTLVRPN	180
Db	121	DMHGDSEYIMFGPDICGPGTKKHVIFNYKGNVLINKDIRCKDDEFTHLYTLVRPN	180
Qy	181	TYEVKIDNSQVSGSLEDNDWFLPPKIKDPASKEPDWDERAKIDDPDTSKPEDWDXE	240
Db	181	TYEVKIDNSQVSGSLEDNDWFLPPKIKDPASKEPDWDERAKIDDPDTSKPEDWDXE	240
Qy	241	HIPDDPAKPEPDWDERAKIDDPDTSKPEDWDXE	300
Db	241	HIPDDPAKPEPDWDERAKIDDPDTSKPEDWDXE	300
Qy	301	PDPSIYAYDNFVGLDLQVKSGLTIFDNLINDEAYAEFGNETGWYTKAAEQMKDK	360
Db	301	PDPSIYAYDNFVGLDLQVKSGLTIFDNLINDEAYAEFGNETGWYTKAAEQMKDK	360
Qy	361	QDEEQRLKEEEDKKKEEEDKEDDEDKEDDEDKEDDEDKEDDEDKEDDEDKEDDEDK	416
Db	361	QDEEQRLKEEEDKKKEEEDKEDDEDKEDDEDKEDDEDKEDDEDKEDDEDKEDDEDK	416

RESULT 2
US-08-675-816-2
; Sequence 2, Application US/08675816
; Patent No. 6171864
; GENERAL INFORMATION:
; APPLICANT: Coughlan, Sean J.
; APPLICANT: Winfrey, Jr., Ron J.
; TITLE OF INVENTION: CALRETICULIN AND CALNEXIN GENES AND PROMOTER REGIONS AND USES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 701 Fifth Ave. Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/675,816
; FILING DATE: 05-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6171864tenburg, Carol
; REGISTRATION NUMBER: 39,317
; REFERENCE/DOCKET NUMBER: 750027.401
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)-622-4900
; TELEFAX: (206)-682-6031
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 415 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-675-816-2

Query Match 53.7%; Score 1224.5; DB 3; Length 415;
Best Local Similarity 55.6%; Pred. No. 3.9e-103;
Matches 232; Conservative 57; Mismatches 109; Indels 19; Gaps 8;
QY 8 LIGLLGLVAEPAVYFKEQFLDGDGWTSRWIESKHSD---FGKFVLSGKFGYDEEKDX 64
DB 11 LLSLLAIASAE--VFEEERF--EDGWNRWKSDWKKDENTAGWNYTSGKWNGD-PNDK 65
QY 65 GLQTSQDARFYALSASFEPFSNKGQTLVVOFTVKHEQNDICGGYVVKLPFNSLDQTDWHG 124
DB 66 GIOTSEDFYFALSAEFPFSNKGQTLVVOFTVKHEQNDICGGYVVKLPFNSLDQTDWHG 125
QY 125 DSEYNIMFGPDICGGTCKVHVIFNYKQVNLINKDRCODEFTHLYTLIVRPNTYEV 184
DB 126 DTPYSIMFGPDICGGTCKVHVIFNYKQVNLINKDRCODEFTHLYTLIVRPNTYEV 185
QY 185 KIDNSQVSGSLEDQWDFLPKKIKDPAKPEDWDERAKIDDPDTSKPEDWDK-PEHIP 243
DB 186 LIDNVEKQTSGLYTDWLLPPKKIDPAKPEDWDERAKIDDPDTSKPEDWDK-PEHIP 245
QY 244 DPDAKPEDWDERAKIDDPDTSKPEDWDK-PEHIP 245
DB 246 DPDAKPEDWDERAKIDDPDTSKPEDWDK-PEHIP 245
QY 304 SIYAYDNFVGLDLWQVSGTIFPNELITNDEAVAEFGNETGWTKAAEKQKQDE 363
DB 306 EIVYVFNLYVGLWQVSGTIFPNELITNDEAVAEFGNETGWTKAAEKQKQDE 362
QY 364 EQLKEEEDKGRKEEBAEDKEDDEDKDEDEEEDKE---EDEEDVPQAKDEL 417
DB 363 AEKKEEESKDDPADSDADEDDDDDDDDTEGDDGESKSDAEDV---HDEL 415

RESULT 3
US-09-828-000-3
; Sequence 3, Application US/09828000
; Patent No. 6596690
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/09/828,000
; CURRENT FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 3
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Vasostatin
US-09-828-000-3
Query Match 42.6%; Score 971; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.4e-80;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 18 EPAYVYFKEQFLDGDGWTSRWIESKHSDFGKFLVSSGKFGYDEEKQGLQTSQDARFYAL 77
DB 1 EPAYVYFKEQFLDGDGWTSRWIESKHSDFGKFLVSSGKFGYDEEKQGLQTSQDARFYAL 60
QY 78 SASPEPFSNKGQTLVVOFTVKHEQNDICGGYVVKLPFNSLDQTDWHGDSYNNIMFGPDIC 137
DB 61 SASPEPFSNKGQTLVVOFTVKHEQNDICGGYVVKLPFNSLDQTDWHGDSYNNIMFGPDIC 120
QY 138 GPQTKKVHVIFNYKQVNLINKDRCODEFTHLYTLIVRPNTYEVKIDNSQVSGSLE 197
DB 121 GPQTKKVHVIFNYKQVNLINKDRCODEFTHLYTLIVRPNTYEVKIDNSQVSGSLE 180
RESULT 4
US-08-296-362-2
; Sequence 2, Application US/08296362
; Patent No. 5691306
; GENERAL INFORMATION:
; APPLICANT: Bergeron, John J.M.
; APPLICANT: Thomas, David Y.
; APPLICANT: Wada, Ikko
; TITLE OF INVENTION: METHODS OF DETECTION AND TREATMENT OF
; TITLE OF INVENTION: PROTEIN TRAFFICKING DISORDERS AND INCREASING SECRETORY
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/296,362
; FILING DATE: 25-AUG-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Deehr, Manya S.
; REGISTRATION NUMBER: 37,120
; REFERENCE/DOCKET NUMBER: 690066.401C1
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 593 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-296-362-2

Query Match 35.0%; Score 799; DB 1; Length 593;
Best Local Similarity 34.9%; Pred. No. 3.4e-64;
Matches 182; Conservative 72; Mismatches 133; Indels 134; Gaps 16;

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QY 21 VYKQFLDGDGWTSRWIESKHSD-----FGKFLVSGKPYGDEEK-----DKGLQTS 69
DB 70 VYFAUSF--DRGLSGWLSKAKDDTDDEIAK---DGKWEVDMEKTKLPDGLGLVM 124
QY 70 QDARYALSASF--EPFSNKGQTLVVQFTVKEQNIQCGGYVKLFPN-----SLDQDMHG 124
DB 125 SRAKHRA-SAKLNKFLFDTKPLIVQYEVNFQNGIECGGAYVKKLSKTPSLNLDQ--FHD 182
QY 125 DSEYINMGPDICGPTKVVHVIENYKGNVLINKDIRCK-----DDEFTHLYTL 174
DB 183 KPYTIMFGPKDCGE-DYKLHPIFRHKPKTGTVFEKKAAPDADLKYTFDCKTHLYTL 241
QY 175 IVRPNTYEVKIDNSQVSGSLEDWDFLPP-----KKIKPDASKPEDWDERAKIDDPD 230
DB 242 ILNPDNSPEILLVDQIVANSGLN--DMTPVNPSSREIEDPDQKPEDWDERPKIPDPDA 299
QY 231 SKPEDW-----DKPEHIDPDPAKPEDWDEMDGSEWEP-----263
DB 300 VKPDDWNEDAPAKIDPEATPDGMLDDEPEYVDPDAKPEDWDEMDGSEWEPAPQIANP 359
QY 264 -----PVIONPEYKGEWKPRQIDNPYKGTWHPHIDNPYSPDPSIYAYDN 310
DB 360 KCESAPGCGVMQRPMDNPNYKGVKPKPMIDNPNYQGLWPKPIPNDFDLEPPQWTP 419
QY 311 FGVLGLDQVKGSGTIFDNFLITNDEAYAEFGNETGVTKAAE-----KOMKDKQD 362
DB 420 FSAIGLELWSMTSDIFFDNFVCGDRRVYDDWANDGMLKKAAGAAEPGVVGQMTAAE 479
QY 363 E-----EORLKEEEDK-----KR 376
DB 480 ERPLWVYVYVVALPVFLVISFCGSKKQSPVEYKTKTAPQPDVKEEKEEEDKDG 539
QY 377 KEEBAEDKEDDEDDEEEDKEEEDKEEEDKEEEDKEEEDKEEEDKEEEDKEEEDKEEED 417
DB 540 DEEEGEKLEEKQKSDAEDPGGTASQEDDRKPAEDEI 580
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RESULT 5

US-09-976-594-947
; Sequence 947, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 947
; LENGTH: 610
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No. 6673549 3876162CD1
US-09-976-594-947

Query Match 32.1%; Score 731.5; DB 4; Length 610;

Best Local Similarity 33.5%; Pred. No. 4.9e-58;
Matches 172; Conservative 82; Mismatches 135; Indels 125; Gaps 16;

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QY 21 VYKQFLDGDGWTSRWIESKHSD--FGKFLVSGKPYGDEEK-----DKGLQTSQDA 72
DB 60 VYFAETP--DSGLAGWLSKAKDDDEISIIYDGRWEIEELKENQVPGDGLVLSRA 117
QY 73 RYVALSASF--EPFSNKGQTLVVQFTVKEQNIQCGGYVKLFPNSLD--QTMHGDSY 123
DB 118 KHAISAVLAKPFIADKPLIVQYEVNFQDIDCGGAYIKLLADTDLLILENFYDKTSYI 177
QY 130 IMFGPDICGPTKVVHVIENYKGNVLINKDIRCK-----DDEFTHLYTLIVRPD 179
DB 178 IMFGDKDCGE-DYKLHPIFRHKPKTGTVFEKKAAPDVLKXFFTDKTHLYTLVWNP 236
QY 180 NTYEVKIDNSQVSGSLEDW--DFLPPKIKPDASKPEDWDERAKIDDPDTSKPEDW- 236
DB 237 DTFEVLVDQTVVNGSLEDVVPPIKPKPEIEDPNDKKPEWDERAKIPDPSAVKPEDWD 296
QY 237 -----DKPEHIDPDPAKPEDWDEMDGSEW-----262
DB 297 ESEPAQIEDSVVPAAGWLDDEPKFIPDPAEKPDWNETDGEWEAPQILNACRIGCG 356
QY 263 ---PVIONPEYKGEWKPRQIDNPYKGTWHPHIDNPYSPDPSIYAYDNFGVLGLDW 319
DB 357 EWKPPMIDNPNYKGVWRPPLVDNPNYQGLWPKPIPNDFDLEPPQWTP 416
QY 320 QVKSQTIIDNELLITNDEAYAEFGNETW-----GVTK-----AAE-----354
DB 417 SMTSDIYDFNFIISKEVADHWAAAGWRKIMIANANKPGVLKQMAAAGHPWMLIY 476
QY 355 -----KOMKDKQDEEOR-----LKEEEDKKEEED-----380
DB 477 LVTAGVPIALITSPCWPRKVKKKHKDTYKTKDICIPTQKGVLEQEEKEEKALEKPM 536
QY 381 EAEDKEDDED--KOEDDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDEDE 412
DB 537 EEEKQNDGEMLEKEEESSESESESESESESESESESESESESESESESESESESESE 570
```

RESULT 6

US-08-675-816-6
; Sequence 6, Application US/08675816
; Patent No. 6171864
; GENERAL INFORMATION:
; APPLICANT: Coughlan, Sean J.
; TITLE OF INVENTION: CALRETICULIN AND CALNEXIN GENES AND PROMOTER REGIONS AND USES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 701 Fifth Ave. Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/675,816
; FILING DATE: 05-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6171864tenburg, Carol
; REGISTRATION NUMBER: 39,317
; REFERENCE/DOCKET NUMBER: 750027.401
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)-622-4900
; TELEFAX: (206)-682-6031
; INFORMATION FOR SEQ ID NO: 6:


```

1 Sequence 2, Application US/08728323A
2 Patent No. 5948676
3 GENERAL INFORMATION:
4 APPLICANT: Chang, Yuan
5 APPLICANT: Bohenzky, Roy A.
6 APPLICANT: Russo, James J.
7 APPLICANT: Edelman, Isidore S.
8 APPLICANT: Moore, Patrick S.
9 TITLE OF INVENTION: Immediate Early Protein From Kaposi's
10 TITLE OF INVENTION: Sarcoma-Associated Herpesvirus, DNA
11 TITLE OF INVENTION: Encoding Same And Uses Thereof
12 NUMBER OF SEQUENCES: 21
13 CORRESPONDENCE ADDRESS:
14 ADDRESS: Cooper & Dunham LLP
15 STREET: 1185 Avenue of the Americas
16 CITY: New York
17 STATE: New York
18 COUNTRY: U.S.A.
19 ZIP: 10036
20 COMPUTER READABLE FORM:
21 MEDIUM TYPE: Floppy disk
22 COMPUTER: IBM PC compatible
23 OPERATING SYSTEM: PC-DOS/MS-DOS
24 SOFTWARE: PatentIn Release #1.0, Version #1.30
25 CURRENT APPLICATION DATA:
26 APPLICATION NUMBER: US/08/728,323A
27 FILING DATE:
28 CLASSIFICATION: 435
29 ATTORNEY/AGENT INFORMATION:
30 NAME: Whice, John P.
31 REGISTRATION NUMBER: 28,678
32 REFERENCE/POCKET NUMBER: 0575/52368/JPW/MSC/SKS
33 TELECOMMUNICATION INFORMATION:
34 TELEPHONE: 212-278-0400
35 TELEFAX: 212-391-0525
36 INFORMATION FOR SEQ ID NO: 2:
37 SEQUENCE CHARACTERISTICS:
38 LENGTH: 1162 amino acids
39 TYPE: amino acid
40 TOPOLOGY: linear
41 MOLECULE TYPE: protein
42 US-08-728-323A-2

```

RESULT 13
US-08-728-323A-2

RESULT 14
US-09-298-568-2
; Sequence 2, Application US/09298568
; Patent No. 6322792
; GENERAL INFORMATION:

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 4, 2004, 12:50:22 ; Search time 46.2882 Seconds
(without alignments)
372.349 Million cell updates/sec

Title: US-09-807-148-5

Perfect score: 327

Sequence: 1 CGPGTKKHVIFVYKGNVL.....PDNTYEVKIDNSQVESGSL 61

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A: Genesep29Jan04.*
1: Genesep1980s.*
2: Genesep1990s.*
3: Genesep2000s.*
4: Genesep2001s.*
5: Genesep2002s.*
6: Genesep2003ast.*
7: Genesep2003bs.*
8: Genesep2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	327	100.0	61	3	AA92352
2	327	100.0	180	3	AA92351 Human vas
3	327	100.0	400	3	AA92350 Recombina
4	327	100.0	401	2	AAW11156 Calreticu
5	327	100.0	416	7	AD56306 Rat Prote
6	327	100.0	416	7	AD56310 Rat Prote
7	327	100.0	417	1	AA92276 60 kD RC
8	327	100.0	417	2	AA90927 Calreticu
9	327	100.0	417	3	AA92349 Human MBP
10	327	100.0	417	5	AAU7712 Human cal
11	327	100.0	417	5	AAE24591 Human cal
12	327	100.0	417	5	AAE18851 Human cal
13	327	100.0	417	5	AB82384 Human cal
14	327	100.0	417	6	ABJ19766 Human MP2
15	327	100.0	417	6	AA92349 Human MBP
16	327	100.0	417	6	ADA26337 Human cal
17	327	100.0	417	7	ADD2407 HLA-B45 T
18	327	100.0	417	7	AD56308 Human Pro
19	327	100.0	417	7	AD56312 Human Pro
20	318	97.2	60	3	AA92354 Recombina
21	318	97.2	280	3	AA92355 Recombina
22	280	85.6	403	2	AAW04171 Flea calr
23	278	85.0	406	4	AB86414 Drosophil
24	258	78.9	49	3	AA92353 Recombina
25	251	76.8	336	2	AAI12312 Partial s

26	190	58.1	122	2	AA900926
27	190	58.1	122	2	AA900924
28	186	56.9	415	4	AA866343
29	186	56.9	415	4	AA866341
30	185	56.6	419	7	ABM74155 DNA clone
31	184	56.3	385	3	AA832385 Human sec
32	184	56.3	390	6	ABO07134 Novel hum
33	182	55.7	122	2	AA900925 Mouse ccl
34	180	55.0	428	7	ABM74288 DNA clone
35	178	54.4	312	3	AA847933 Arabidops
36	178	54.4	312	3	AA847933 Arabidops
37	178	54.4	332	3	AA830998 Arabidops
38	178	54.4	421	3	AA824608 Arabidops
39	178	54.4	421	3	AA824608 Arabidops
40	178	54.4	424	3	AA824607 Arabidops
41	178	54.4	424	3	AA824607 Arabidops
42	178	54.4	441	3	AA830997 Arabidops
43	178	54.4	444	3	AA830996 Arabidops
44	170	52.0	420	5	ABB04656 Maize cal
45	117.5	35.9	592	4	ABB44554 Human wou

ALIGNMENTS

RESULT 1

AA92352
ID AA92352 standard; protein; 61 AA.

XX AC AA92352;

XX DT 10-AUG-2000 (first entry)

XX DE Recombinant human calreticulin residues 120-180.

XX KW MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;

XX KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;

XX KW cytostatic; dermalogical; immunosuppressive; antiinflammatory; hepatic;

XX KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.

XX OS Homo sapiens.

XX OS Synthetic.

XX WO200020577-A1.

XX PD 13-APR-2000.

XX PF 05-OCT-1999; 99WO-US023240.

XX PA 06-OCT-1998; 98US-0103438P.

XX PI (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PI Tosato G, Pike SE, Yao L;

XX DR WPI; 2000-303767/26.

XX PT Inhibiting endothelial cell growth and angiogenesis using calreticulin,

XX PS useful for suppressing tumor growth.

XX PS Claim 4; Page 82-83; 99pp; English.

XX CC A novel method of inhibiting endothelial cell growth comprises contacting the cells with calreticulin (or its fragments/variants). Fragments of calreticulin causes at least 40% inhibition of angiogenesis, tumor growth and/or endothelial cell growth (claimed). The method may be used for inhibiting angiogenesis in a patient. The angiogenesis is associated with a disease other than a tumor that is associated with neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia, trachoma, neovascular glaucoma, psoriasis, angiodiomas, immune inflammation, atherosclerosis, excessive wound repair, retinal neovascularization, macular degeneration, corneal graft rejection, contact lens overwear, Crohn's disease, non-immune inflammation, rheumatoid arthritis, systemic

CC lupus erythromatosus, thyroiditis, Goodpasture's syndrome, systemic
 CC vasculitis, scleroderma, Sjorgen's syndrome, sarcoidosis and primary
 CC biliary cirrhosis). The method may also be used for treating/inhibiting
 CC tumor growth especially Kaposi's sarcoma (claimed)
 XX SQ Sequence 61 AA;
 Query Match 100.0%; Score 327; DB 3; Length 61;
 Best Local Similarity 100.0%; Pred. No. 3.3e-38;
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGPGTKKVVHVFNYKGNVLINKDRCCKDETHLYTLVIRPDNTYEVKIDNSQVESGSL 60
 DB 1 CGPGTKKVVHVFNYKGNVLINKDRCCKDETHLYTLVIRPDNTYEVKIDNSQVESGSL 60
 QY 61 E 61
 DB 61 E 61
 RESULT 2
 AAY92351
 ID AAY92351 standard; protein; 180 AA.
 XX AC AAY92351;
 XX DT 10-AUG-2000 (first entry)
 XX DE Human vasostatin (calreticulin N-terminal 180 amino acids).
 XX KW MBP-calreticulin; maltose binding protein; vasostatin; N-terminal;
 KW angiogenesis; inhibition; endothelial cell; anti-angiogenic;
 KW neuroprotective; antidiabetic; cytostatic; dermatological; hepatic;
 KW immunosuppressive; antiinflammatory; anti-atherosclerotic;
 KW gastrointestinal; anti-arthritis; ophthalmic.
 XX OS Homo sapiens.
 OS Synthetic.
 XX PN WO200020577-A1.
 XX PD 13-APR-2000.
 XX PF 05-OCT-1999; 99WO-US023240.
 XX PR 06-OCT-1998; 98US-0103438P.
 XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX PI Tosato G, Pike SE, Yao L;
 XX DR WPI; 2000-303767/26.
 XX PT Inhibiting endothelial cell growth and angiogenesis using calreticulin,
 XX useful for suppressing tumor growth.
 XX PS Claim 4; Page 82; 99pp; English.
 CC A novel method of inhibiting endothelial cell growth comprises contacting
 CC the cells with calreticulin (or its fragments/variants). Fragments of
 CC calreticulin causes at least 40% inhibition of angiogenesis, tumor growth
 CC and/or endothelial cell growth (claimed). The method may be used for
 CC inhibiting angiogenesis in a patient. The angiogenesis is associated with
 CC a disease other than a tumor that is associated with neovascularization
 CC (e.g. diabetic neuropathy, retrolental fibroplasia, trachoma, neovascular
 CC glaucoma, psoriasis, angiofibromas, immune inflammation,
 CC atherosclerosis, excessive wound repair, retinal neovascularization,
 CC macular degeneration, corneal graft rejection, contact lens overwear,
 CC Crohn's disease, non-immune inflammation, rheumatoid arthritis, systemic
 CC lupus erythromatosus, thyroiditis, Goodpasture's syndrome, systemic
 CC vasculitis, scleroderma, Sjorgen's syndrome, sarcoidosis and primary
 CC biliary cirrhosis). The method may also be used for treating/inhibiting
 CC tumor growth especially Kaposi's sarcoma (claimed)

XX SQ Sequence 180 AA;
 Query Match 100.0%; Score 327; DB 3; Length 180;
 Best Local Similarity 100.0%; Pred. No. 1.3e-37;
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGPGTKKVVHVFNYKGNVLINKDRCCKDETHLYTLVIRPDNTYEVKIDNSQVESGSL 60
 DB 120 CGPGTKKVVHVFNYKGNVLINKDRCCKDETHLYTLVIRPDNTYEVKIDNSQVESGSL 179
 QY 61 E 61
 DB 180 E 180
 RESULT 3
 AAY92350
 ID AAY92350 standard; protein; 400 AA.
 XX AC AAY92350;
 XX DT 10-AUG-2000 (first entry)
 XX DE Recombinant human MBP-calreticulin.
 XX KW MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;
 KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
 KW cytostatic; dermatological; immunosuppressive; antiinflammatory; hepatic;
 KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.
 XX OS Homo sapiens.
 XX DN WO200020577-A1.
 XX PD 13-APR-2000.
 XX PF 05-OCT-1999; 99WO-US023240.
 XX PR 06-OCT-1998; 98US-0103438P.
 XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX PI Tosato G, Pike SE, Yao L;
 XX DR WPI; 2000-303767/26.
 XX PR N-PSDB; AAA09346, AAA09347.
 XX PT Inhibiting endothelial cell growth and angiogenesis using calreticulin,
 XX useful for suppressing tumor growth.
 XX PS Claim 4; Page 80-81; 99pp; English.
 CC Recombinant human MBP-calreticulin comprises the sequence of human
 CC calreticulin (see AAY92349) without the 17 N-terminal amino acids. A
 CC novel method of inhibiting endothelial cell growth comprises contacting
 CC the cells with calreticulin (or its fragments/variants). Fragments of
 CC calreticulin causes at least 40% inhibition of angiogenesis, tumor growth
 CC and/or endothelial cell growth (claimed). The method may be used for
 CC inhibiting angiogenesis in a patient. The angiogenesis is associated with
 CC a disease other than a tumor that is associated with neovascularization
 CC (e.g. diabetic neuropathy, retrolental fibroplasia, trachoma, neovascular
 CC glaucoma, psoriasis, angiofibromas, immune inflammation,
 CC atherosclerosis, excessive wound repair, retinal neovascularization,
 CC macular degeneration, corneal graft rejection, contact lens overwear,
 CC Crohn's disease, non-immune inflammation, rheumatoid arthritis, systemic
 CC lupus erythromatosus, thyroiditis, Goodpasture's syndrome, systemic
 CC vasculitis, scleroderma, Sjorgen's syndrome, sarcoidosis and primary
 CC biliary cirrhosis). The method may also be used for treating/inhibiting
 CC tumor growth especially Kaposi's sarcoma (claimed)
 XX SQ Sequence 400 AA;

Query Match 100.0%; Score 327; DB 3; Length 400;
 Best Local Similarity 100.0%; Pred. No. 3.8e-37;
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGPGTKKVVHVFYKGNVLINKDIRCKDDEFTHTLTVLRPNTYEVKIDNSQVSGSL 60
 DB 120 CGPGTKKVVHVFYKGNVLINKDIRCKDDEFTHTLTVLRPNTYEVKIDNSQVSGSL 179

QY 61 E 61
 DB 180 E 180

RESULT 4
 ID AAW11156 standard; peptide; 401 AA.
 AC AAW11156;
 DT 31-MAY-1997 (first entry)
 DE Calreticulin.
 KW calreticulin; C-domain; restenosis; inhibitor.
 OS Homo sapiens.
 FN WO9636643-A1.
 PD 21-NOV-1996.
 PF 17-MAY-1996; 96WO-IB000471.
 PR 17-MAY-1995; 95US-00442844.
 PR 16-MAY-1996; 96US-00649417.
 PA (UYAL-) UNIV ALBERTA.
 PI Michalak M, Lucas A;
 DR WPI; 1997-012036/01.
 XX Inhibition of restenosis in patients - using calreticulin or a C-domain
 PT polypeptide of calreticulin or a variant with the same activity.
 PS Disclosure; Fig 1; 48pp; English.
 CC The present sequence is calreticulin. It and a C-domain derived peptide
 CC (AAW06736) are useful for treating a patient to inhibit restenosis. The
 CC calreticulin-type cpds. are administered either parenterally,
 CC intravenously or via a catheter and can target areas of vascular damage
 CC to inhibit or prevent restenosis
 SQ Sequence 401 AA;

Query Match 100.0%; Score 327; DB 2; Length 401;
 Best Local Similarity 100.0%; Pred. No. 3.8e-37;
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGPGTKKVVHVFYKGNVLINKDIRCKDDEFTHTLTVLRPNTYEVKIDNSQVSGSL 60
 DB 120 CGPGTKKVVHVFYKGNVLINKDIRCKDDEFTHTLTVLRPNTYEVKIDNSQVSGSL 179

QY 61 E 61
 DB 180 E 180

RESULT 5
 ID ADE56306 standard; protein; 416 AA.
 XX ADE56306;
 AC ADE56306;

XX 29-JAN-2004 (first entry)
 DT Rat Protein F18418, SEQ ID NO 2158.
 DE Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
 KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
 XX Rattus norvegicus.
 OS WO2003016475-A2.
 FN 27-FEB-2003.
 XX 14-AUG-2002; 2002WO-US025765.
 PF 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX (GEO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 XX Woolf C, D'urso D, Befort K, Costigan M;
 PI WPI; 2003-268312/26.
 DR GENBANK; F18418.
 XX New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 PS Claim 1; Page; 1017pp; English.
 XX The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. gene
 CC injury (CCI) and spared nerve injury (SNI))
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX SQ Sequence 416 AA;

Query Match 100.0%; Score 327; DB 7; Length 416;
 Best Local Similarity 100.0%; Pred. No. 4e-37;
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGPGTKKVVHVFYKGNVLINKDIRCKDDEFTHTLTVLRPNTYEVKIDNSQVSGSL 60
 DB 137 CGPGTKKVVHVFYKGNVLINKDIRCKDDEFTHTLTVLRPNTYEVKIDNSQVSGSL 196

QY 61 E 61

Db 197 E 197

RESULT 6
ADE56310
ID ADE56310 standard; protein; 416 AA.
XX AC ADE56310;
XX DE 29-JAN-2004 (first entry)
XX DT Rat Protein P18418, SEQ ID NO 2162.
XX DE Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
XX KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX OS Rattus norvegicus.
XX PN WO2003016475-A2.
XX PD 27-FEB-2003.
XX PF 14-AUG-2002; 2002WO-US025765.
XX PR 14-AUG-2001; 2001US-0312147P.
XX PR 01-NOV-2001; 2001US-0346382P.
XX PR 26-NOV-2001; 2001US-0333347P.
XX PA (GEMO) GEN HOSPITAL CORP.
XX PA (FARB) BAYER AG.
XX PI Woolf C, D'urso D, Befort K, Costigan M;
XX DR WPI; 2003-268312/26.
XX DR GENBANK; P18418.
XX PT New composition comprising two or more isolated polypeptides, useful for
XX PT preparing a medicament for treating pain in an animal.
XX PS Claim 1; Page; 1017pp; English.
XX CC The invention discloses a composition comprising two or more isolated rat
XX CC or human polynucleotides or a polynucleotide which represents a fragment,
XX CC derivative or allelic variation of the nucleic acid sequence. Also
XX CC claimed are a vector comprising the novel polynucleotide, a host cell
XX CC comprising the vector, a method for identifying a nucleotide sequence
XX CC which is differentially regulated in an animal subjected to pain and a
XX CC kit to perform the method, an array, a method for identifying an agent
XX CC that increases or decreases the expression of the polynucleotide sequence
XX CC that is differentially expressed in neuronal tissue of a first animal
XX CC subjected to pain, a method for identifying a compound which regulates
XX CC the expression of a polynucleotide sequence which is differentially
XX CC expressed in an animal subjected to pain, a method for identifying a
XX CC compound that regulates the activity of one or more of the
XX CC polynucleotides, a method for producing a pharmaceutical composition, a
XX CC method for identifying a compound or small molecule that regulates the
XX CC activity in an animal of one or more of the polypeptides given in the
XX CC specification, a method for identifying a compound useful in treating
XX CC pain and a pharmaceutical composition comprising the one or more
XX CC polypeptides or their antibodies. The polynucleotide or the compound that
XX CC modulates its activity is useful for preparing a medicament for treating
XX CC pain (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. Gene
XX CC therapy). The sequence presented is a rat protein (shown in Table 2 of
XX CC the specification) which is differentially expressed during pain. Note:
XX CC The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic form directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 416 AA;

Query Match 100.0%; Score 327; DB 7; Length 416;
Best Local Similarity 100.0%; Pred. No. 4e-37;

Query Match 100.0%; Score 327; DB 1; Length 417;
Best Local Similarity 100.0%; Pred. No. 4e-37;

Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGPGTKKVHVIFNYKGNVINKDIRCKDDEFTHLTYLIVRPDNTYEVKIDNSQVESGSL 60
DB 137 CGPGTKKVHVIFNYKGNVINKDIRCKDDEFTHLTYLIVRPDNTYEVKIDNSQVESGSL 196
QY 61 E 61
DB 197 E 197

RESULT 7
AAP92276
ID AAP92276 standard; protein; 417 AA.
XX AC AAP92276;
XX DT 25-MAR-2003 (revised)
XX DT 23-FEB-1990 (first entry)
XX DE 60 kD Ro (Ro/SSA) antigen.
XX KW Sjorens syndrome; systemic lupus erythematosus.
XX OS Synthetic.
XX PN WO8909273-A.
XX PD 05-OCT-1989.
XX PF 22-MAR-1989; 89WO-US001213.
XX PR 22-MAR-1988; 88US-00171634.
XX PA (TEXA) UNIV TEXAS SYSTEM.
XX PI Sontheimer RD, Lieu TS, Capra JD, Mccauliffe DP;
XX DR WPI; 1989-309537/42.
XX DR N-PSDB; AAP92276.
XX PT DNA sequences encoding antigenic epitope(s) of RO 60 KD auto-antigen -
XX PT used in immunoassays to detect rheumatic disease.
XX PS Disclosure; Fig 2; 88pp; English.
XX CC Synthetic peptides corresp. to an epitopic core of Ro antigen are
XX CC expressed recombinantly to detect autoantibodies, for identification of
XX CC autoimmune diseases. These epitopes are AAs 24-36, 23-36, 188-209, or 241
XX CC -255. The peptides may be substd. for ribonucleoprotein particle
XX CC antigens. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-
XX CC MAR-2003 to correct PI field.)
XX SQ Sequence 417 AA;

Query Match 100.0%; Score 327; DB 1; Length 417;
Best Local Similarity 100.0%; Pred. No. 4e-37;

Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGPGTKKVHVIFNYKGNVINKDIRCKDDEFTHLTYLIVRPDNTYEVKIDNSQVESGSL 60
DB 137 CGPGTKKVHVIFNYKGNVINKDIRCKDDEFTHLTYLIVRPDNTYEVKIDNSQVESGSL 196
QY 61 E 61
DB 197 E 197

RESULT 8
AAY00927
ID AAY00927 standard; protein; 417 AA.
XX AC AAY00927;

KW cytostatic; vaccine; human papillomavirus 16; HPV 16; E7; DNA vaccine;
 KW enhanced antigen-specific immune response; cytotoxic T lymphocyte;
 KW tumour; cancer; cervical cancer.
 XX Homo sapiens.
 OS
 XX WO200212281-A2.
 PN
 XX
 PD 14-FEB-2002.
 PD
 XX
 PF 02-AUG-2001; 2001WO-US024134.
 XX
 XX 03-AUG-2000; 2000US-0222902P.
 XX
 XX (UWJO) UNIV JOHNS HOPKINS.
 PA
 XX
 PI Wu T, Hung C;
 XX
 XX WPI; 2002-257463/30.
 DR N-PSDB; ABK11662.
 DR
 XX
 XX New nucleic acids encoding a fusion polypeptide comprising an endoplasmic
 PT reticulum chaperone polypeptide linked to an antigenic polypeptide,
 PT useful as a vaccine for inducing antigen-specific immune responses.
 XX
 XX Disclosure; Page 27; 71pp; English.
 PS
 XX The invention describes a nucleic acid molecule (I) encoding a fusion
 CC polypeptide comprising a first polypeptide domain comprising an
 CC endoplasmic reticulum chaperone polypeptide e.g. calreticulin (CRT) and a
 CC second polypeptide domain comprising at least one antigenic peptide e.g.
 CC Human papillomavirus 16 (HPV 16) E7. The nucleic acid is useful as a
 CC vaccine (DNA vaccine) for inducing enhanced antigen-specific immune
 CC responses, particularly those mediated by cytotoxic T lymphocytes. The
 CC nucleic acid and compositions comprising the nucleic acid is also useful
 CC for inhibiting the growth of tumours and cancers e.g. cervical cancer.
 CC This is the amino acid sequence of the human calreticulin (CRT), an
 CC endoplasmic reticulum protein used in the creation of a DNA vaccine
 XX
 SQ Sequence 417 AA;
 Query Match 100.0%; Score 327; DB 5; Length 417;
 Best Local Similarity 100.0%; Pred. No. 4e-37;
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGPGTKKVVHVFNYKGNVLINKDIRCKDDEFTHTLTVLRPDNTYEVKIDNSQVESGSL 60
 DB 137 CGPGTKKVVHVFNYKGNVLINKDIRCKDDEFTHTLTVLRPDNTYEVKIDNSQVESGSL 196
 QY 61 E 61
 DB 197 E 197
 RESULT 11
 AAE24591
 ID AAE24591 standard; protein; 417 AA.
 XX
 AC AAE24591;
 XX
 DT 04-OCT-2002 (first entry)
 XX
 DE Human calreticulin protein.
 XX
 KW Human; calreticulin; antisense compound; hyperproliferative disorder;
 KW cancer; autoimmune disease; viral infection; cardiovascular disease;
 KW antisense therapy; cytostatic; immunosuppressive; virucide.
 XX
 OS Homo sapiens.
 XX
 PN WO200236743-A2.
 XX
 PD 10-MAY-2002.

XX 30-OCT-2001; 2001WO-US049045.
 XX
 PR 30-OCT-2000; 2000US-00702327.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Bennett CF, Cowser LM;
 XX
 DR WPI; 2002-479759/51.
 DR N-PSDB; AAD39469.
 XX
 PT Novel antisense compound targeted to nucleic acid encoding calreticulin,
 PT useful for treating a human having disease or condition associated with
 PT calreticulin e.g. cancer, viral infection, autoimmune disease.
 XX
 PS Disclosure; Page 88-90; 109pp; English.
 CC
 CC The invention relates to antisense compounds, compositions and methods
 CC for modulating the expression of calreticulin. The compositions comprise
 CC antisense compounds, particularly antisense oligonucleotides, targeted
 CC to nucleic acids encoding calreticulin. The antisense compound is useful
 CC for inhibiting the expression of calreticulin in human cells or tissues.
 CC It is also useful for treating a human having a disease or condition
 CC associated with calreticulin, e.g., hyperproliferative disorder e.g.
 CC cancer, autoimmune disease, viral infection or cardiovascular disease, by
 CC inhibiting expression of calreticulin. It is useful for diagnostics,
 CC therapeutics, prophylaxis and as research reagents and kits. It is also
 CC used in antisense therapy. The present sequence is human calreticulin
 CC protein. This sequence is used in the exemplification of the invention
 XX
 SQ Sequence 417 AA;
 Query Match 100.0%; Score 327; DB 5; Length 417;
 Best Local Similarity 100.0%; Pred. No. 4e-37;
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGPGTKKVVHVFNYKGNVLINKDIRCKDDEFTHTLTVLRPDNTYEVKIDNSQVESGSL 60
 DB 137 CGPGTKKVVHVFNYKGNVLINKDIRCKDDEFTHTLTVLRPDNTYEVKIDNSQVESGSL 196
 QY 61 E 61
 DB 197 E 197
 RESULT 12
 AAE18851
 ID AAE18851 standard; protein; 417 AA.
 XX
 AC AAE18851;
 XX
 DT 17-MAY-2002 (first entry)
 XX
 DE Human calreticulin protein.
 XX
 KW Human; prostate cancer; calreticulin; T1D-1 protein; TRAITS protein;
 KW androgen action pathway; cell proliferation; kidney cancer; lymphoma;
 KW epithelium-derived carcinoma; leukaemia; vaccine; gene therapy;
 KW cytostatic; U19 protein.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 98..170
 FT /label= N-terminal_domain
 FT Region 98..103
 FT /label= Alpha_helix
 FT Region 149..154
 FT /label= Alpha_helix
 FT Domain 171..285
 FT /note= "Proline-rich domain (P domain)"
 FT Domain 286..397

FT XX /label= C-terminal_domain
 PN WO200206327-A2.
 XX
 PD 24-JAN-2002.
 XX
 PF 17-JUL-2001; 2001WO-US022357.
 XX
 PR 17-JUL-2000; 2000US-0218761P.
 PR 16-JUL-2001; 2001US-00906393.
 XX
 PA (NOUN) UNIV NORTHWESTERN.
 XX
 XX Wang Z, Xiao W;
 PI
 XX WPI; 2002-179780/23.
 DR N-PSDB; AAD29931.
 XX
 XX Identifying a subject that is likely to have aggressive form of prostate
 PT cancer, involves comparing calreticulin levels in prostate specimen of
 PT the subject and in benign prostatic epithelial cells of the same subject.
 XX
 PS Disclosure; Page 146-149; 148pp; English.
 XX
 CC The present invention relates to methods of distinguishing aggressive
 CC forms of prostate cancer from non-aggressive forms. The method involves
 CC comparing the level of calreticulin in prostate specimen and in benign
 CC prostatic epithelial cells of a subject. The invention particularly
 CC relates to two proteins, namely calreticulin and TID-1 (TRAITS; UI3) that
 CC are down-regulated in aggressive forms of prostate cancer but not in
 CC slowly progressing prostate cancer. They play important roles in the part
 CC of androgen action pathway that suppresses cell proliferation and/or
 CC prevents prostate cancer. The method is useful for identifying a subject
 CC who is likely to have an aggressive form of prostate cancer. The
 CC invention further relates to a method of identifying a subject with a
 CC slow growing form of prostate cancer. TID-1 sequences are useful for
 CC treating cancers such as epithelium-derived carcinomas, kidney cancers,
 CC lymphomas, leukaemias and prostate cancers. Sequences of the invention
 CC are used as vaccines and in gene therapy. The present sequence is human
 CC calreticulin protein
 XX
 SQ Sequence 417 AA;
 Query Match 100.0%; Score 327; DB 5; Length 417;
 Best Local Similarity 100.0%; Pred. No. 4e-37;
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGPGTKKVHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTVEVKIDNSQVSGSL 60
 DB 137 CGPGTKKVHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTVEVKIDNSQVSGSL 196
 QY 61 E 61
 DB 197 E 197
 RESULT 13
 ABB82384
 ID ABB82384 standard; protein; 417 AA.
 XX
 AC ABB82384;
 XX
 DT 08-JAN-2003 (first entry)
 XX
 DE Human calreticulin (CRT) protein.
 XX
 KW Immunogenicity; cytostatic; virucide; protozoacide; antibacterial; CTL;
 KW hepatotropic; anti-HIV; vaccine. cytotoxic T lymphocyte; tumour; CRT;
 KW calreticulin; human.
 XX
 OS Homo sapiens.
 XX
 PN WO200274920-A2.

XX 26-SEP-2002.
 PD
 XX 18-MAR-2002; 2002WO-US008033.
 PF
 XX 16-MAR-2001; 2001US-0276854P.
 PR
 XX (UYJO) UNIV JOHNS HOPKINS.
 PA
 XX Wu T, Hung C;
 PI
 XX WPI; 2002-740856/80.
 DR N-PSDB; ABV73173.
 XX
 PT New nucleic acid molecule encoding an antigenic fusion polypeptide useful
 PT as vaccines for enhancing or inducing immune responses, primarily
 PT cytotoxic T lymphocytes (CTL) responses to specific antigens such as
 PT tumor or viral antigens.
 XX
 PS Disclosure; page 27; 93pp; English.
 XX
 CC The invention relates to a nucleic acid molecule that encodes a fusion
 CC polypeptide, comprising a first nucleic acid sequence encoding a
 CC polypeptide that comprises at least one immunogenicity-potentiating
 CC polypeptide, optionally, fused in frame with the nucleic acid, a linker
 CC nucleic acid encoding a linker peptide, and a nucleic acid that is linked
 CC in frame to them, and that encodes an antigenic peptide or polypeptide.
 CC The nucleic acid molecule, polypeptides and vectors are useful as
 CC vaccines for enhancing immune responses, primarily cytotoxic T
 CC lymphocytes (CTL) responses to specific antigens such as tumour or viral
 CC antigens, and for inhibiting growth or preventing re-growth of a tumour.
 CC The packaging cell line is useful for generating alphavirus replicon
 CC particles without contamination from replicon-competent virus. The
 CC pathogenic organisms include viruses such as human papilloma virus (HPV),
 CC hepatitis B virus, hepatitis C virus, human immunodeficiency virus,
 CC Epstein Barr virus and herpes simplex virus, intracellular parasites such
 CC as malaria, and bacteria that grow intracellularly such as mycobacteria
 CC and listeria. The present sequence represents a human calreticulin (CRT)
 XX
 SQ Sequence 417 AA;
 Query Match 100.0%; Score 327; DB 5; Length 417;
 Best Local Similarity 100.0%; Pred. No. 4e-37;
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGPGTKKVHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTVEVKIDNSQVSGSL 60
 DB 137 CGPGTKKVHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTVEVKIDNSQVSGSL 196
 QY 61 E 61
 DB 197 E 197
 RESULT 14
 ABB19766
 ID ABB19766 standard; protein; 417 AA.
 XX
 AC ABB19766;
 XX
 DT 03-APR-2003 (first entry)
 XX
 DE Human MP21 protein CRTC SEQ ID No 46.
 XX
 KW Cytostatic; p21 pathway modulating agent; cancer; angiogenic; apoptotic;
 KW cell proliferation disorder; MP21.
 XX
 OS Homo sapiens.
 XX
 PN WO2003006990-A1.
 XX
 PD 23-JAN-2003.
 XX

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PF 10-JUL-2002; 2002WO-US021549.
XX
XX 12-JUL-2001; 2001US-0305017P.
PR 10-OCT-2001; 2001US-0328431P.
PR 15-FEB-2002; 2002US-0357452P.
XX
XX (EXEL-) EXELIXIS INC.
PA
XX
XX Friedman L, Plowman GD, Belvin M, Li D, Funke RP;
PI
XX
XX WPI; 2003-221779/21.
DR
XX
XX N-PSDB; ABT17040.
XX
XX
XX Identifying candidate p21 pathway modulator, by contacting an assay
PT system having modifiers of p21 polypeptide or gene with a test agent to
PT provide a reference activity in system and detecting test agent-biased
PT activity.
XX
XX Example; Page 153-155; 199pp; English.
PS
XX
XX The invention relates to a novel method for identifying a candidate p21
CC pathway modulating agent. The novel method comprises contacting an assay
CC system, comprising a purified p21 polypeptide (modifier of p21) or
CC nucleic acid, with a test agent under conditions, so that but for the
CC presence of a test agent the assay system provides a reference activity
CC and detection of test agent-biased activity of the assay system. The
CC novel method of the invention is useful for identifying a candidate p21
CC pathway modulating agent. The invention also includes a method for
CC modulating the p21 pathway of a cell, and a method for diagnosing a
CC disease e.g. cancer in a patient. The identified modulators are useful in
CC diagnosis, therapy and pharmaceutical development. The modulators are
CC useful in a variety of diagnostic and therapeutic applications including
CC angiogenic, apoptotic and cell proliferation disorders. This sequence
CC represents an MP21 protein of the invention
XX
XX Sequence 417 AA;
XX
XX Query Match 100.0%; Score 327; DB 6; Length 417;
XX Best Local Similarity 100.0%; Pred. No. 4e-37;
XX Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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XX QY 1 CGPGTKKHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSL 60
XX |
XX Db 137 CGPGTKKHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSL 196
XX |
XX QY 61 E 61
XX |
XX Db 197 E 197
XX
XX RESULT 15
XX AAG79824
XX ID AAG79824 standard; protein; 417 AA.
XX
XX AC AAG79824;
XX
XX DT 16-APR-2003 (first entry)
XX
XX DE Calreticulin.
XX
XX KW Motif; SE; signal transduction; Alzheimer's disease; neuronal cell;
XX Calreticulin; arrhythmia; idiopathic nephritic syndrome;
XX non-autoimmune hyperthyroidism; obesity; polycystic kidney disease;
XX cancer; asthma; atopic dermatitis; psoriasis; rheumatoid arthritis;
XX systemic lupus erythematosus; infectious disease; atherosclerosis;
XX inflammatory bowel disease; osteoarthritis; septic shock;
XX congestive heart failure; insulin-resistance syndrome;
XX ischaemia-reperfusion injury.
XX
XX OS Homo sapiens.
XX
XX PN WO200299061-A2.
XX
XX

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PD 12-DEC-2002.
XX
XX 04-JUN-2002; 2002WO-US017536.
XX
XX 04-JUN-2001; 2001US-0295691P.
PR
XX 03-JUN-2002; 2002US-00161959.
XX
XX (UNMI ) UNIV MICHIGAN.
PA
XX
XX Holoshitz J, Ling S;
PI
XX
XX WPI; 2003-156853/15.
DR
XX
XX Treating diseases associated with signal transduction aberrations, e.g.
PT Alzheimer's disease, arrhythmia or rheumatoid arthritis, comprises
PT administering a preparation comprising an SE- or an SE motif-containing
PT peptide.
XX
XX Disclosure; Fig 14; 97pp; English.
PS
XX
XX This sequence represents human calreticulin. This protein was used in the
CC method of the invention for treating diseases associated with signal
CC transduction aberrations. The method comprises: (a) providing a subject
CC with one or more symptoms of Alzheimer's disease and, optionally, a
CC plurality of neuronal cells expressing calreticulin, and a preparation
CC comprising an shared epitope (SE) - containing peptide or a peptide which
CC binds the calreticulin; and (b) administering the preparation to the
CC subject. The inventive method is useful for treating diseases associated
CC with signal transduction aberrations, such as Alzheimer's disease,
CC arrhythmia, idiopathic nephritic syndrome, non-autoimmune
CC hyperthyroidism, obesity, polycystic kidney disease, cancer, asthma,
CC atopic dermatitis, psoriasis, rheumatoid arthritis, systemic lupus
CC erythematosus, infectious diseases, inflammatory bowel disease,
CC osteoarthritis, septic shock, atherosclerosis, congestive heart failure,
CC insulin-resistance syndrome, and ischaemia-reperfusion injury
XX
XX Sequence 417 AA;
XX
XX Query Match 100.0%; Score 327; DB 6; Length 417;
XX Best Local Similarity 100.0%; Pred. No. 4e-37;
XX Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 CGPGTKKHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSL 60
XX |
XX Db 137 CGPGTKKHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSL 196
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XX QY 61 E 61
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XX Db 197 E 197
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XX Search completed: October 4, 2004, 13:03:31
XX Job time : 48.2882 secs

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OM protein - protein search, using sw model

Run on: October 4, 2004, 13:01:22 ; Search time 13.6353 Seconds
(without alignments)
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Title: US-09-807-148-5

Perfect score: 327

Sequence: 1 CGPGTKKVHVFNYKGNVL.....PDNTYEVKIDNSQVSGSL 61

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents AA.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	327	100.0	61	4	US-09-828-000-8
2	327	100.0	180	4	US-09-828-000-3
3	327	100.0	416	4	US-09-828-000-2
4	244	74.6	61	4	US-09-828-000-4
5	189	57.8	35	4	US-09-828-000-7
6	186	56.9	415	3	US-08-675-816-2
7	151	46.2	27	4	US-09-828-000-5
8	115.5	35.3	593	1	US-08-296-362-2
9	107.5	32.9	610	4	US-09-976-594-947
10	96	29.4	18	4	US-09-828-000-6
11	82.5	25.2	542	3	US-08-675-816-5
12	61.5	18.8	582	3	US-08-908-865-3
13	61.5	17.6	126	4	US-09-129-668-3
14	57.5	16.8	588	4	US-09-732-210-1163
15	55	16.8	588	4	US-09-252-991A-18861
16	54.5	16.7	410	2	US-08-723-415B-10
17	54.5	16.7	410	3	US-09-189-627A-10
18	54.5	16.7	410	4	US-09-710-861-10
19	54	16.5	405	1	US-07-828-954-2
20	54	16.5	405	1	US-07-994-423-2
21	54	16.5	405	1	US-08-421-891-2
22	54	16.5	474	4	US-09-134-001C-3176
23	54	16.5	816	1	US-08-190-802A-54
24	54	16.5	816	3	US-08-477-346-54
25	54	16.5	816	4	US-08-473-089-54
26	54	16.5	816	4	US-08-487-072A-54
27	54	16.5	1009	4	US-09-693-146-4

28 53.5 16.4 279 2 US-08-701-191A-23 Sequence 23, Appl
29 53.5 16.4 279 4 US-09-564-526-23 Sequence 23, Appl
30 53.5 16.4 355 1 US-08-292-549-6 Sequence 6, Appl
31 53.5 16.4 355 3 US-09-006-353A-14 Sequence 14, Appl
32 53.5 16.4 355 4 US-09-573-986-14 Sequence 14, Appl
33 53.5 16.4 812 1 US-08-446-794A-4 Sequence 4, Appl
34 53.5 16.4 943 4 US-09-540-236-3458 Sequence 3458, Ap
35 53.5 16.4 984 2 US-08-673-789-9 Sequence 9, Appl
36 53.5 16.4 984 2 US-08-449-645A-19 Sequence 19, Appl
37 53.5 16.4 984 2 US-08-702-367A-19 Sequence 19, Appl
38 53.5 16.4 984 5 PCT-US95-04681-13 Sequence 19, Appl
39 53 16.2 91 4 US-09-134-001C-2369 Sequence 2369, Ap
40 53 16.2 410 2 US-08-723-415B-11 Sequence 11, Appl
41 53 16.2 410 2 US-08-428-131-2 Sequence 2, Appl
42 53 16.2 410 3 US-08-602-846-2 Sequence 2, Appl
43 53 16.2 410 3 US-09-078-596-2 Sequence 11, Appl
44 53 16.2 410 3 US-09-189-627A-11 Sequence 11, Appl
45 53 16.2 410 4 US-09-710-861-11 Sequence 11, Appl

ALIGNMENTS

RESULT 1

US-09-828-000-8

; Sequence 8, Application US/09828000

; Patent No. 6596890

; GENERAL INFORMATION:

; APPLICANT: Government of the United States of America

; TITLE OF INVENTION: Vasostatin as Marrow Protectant

; FILE REFERENCE: 4239-55414

; CURRENT APPLICATION NUMBER: US/09/828,000

; CURRENT FILING DATE: 2001-04-06

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 8

; LENGTH: 61

; TYPE: PRT

; ORGANISM: Fragment 5

US-09-828-000-8

Query Match 100.0%; Score 327; DB 4; Length 61;

Best Local Similarity 100.0%; Pred. No. 2.5e-37;

Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGPGTKKVHVFNYKGNVLINKDIRCKDDEFTLYTLIVRPDNTYEVKIDNSQVSGSL 60

Db 1 CGPGTKKVHVFNYKGNVLINKDIRCKDDEFTLYTLIVRPDNTYEVKIDNSQVSGSL 60

Qy 61 E 61

Db 61 E 61

RESULT 2

US-09-828-000-3

; Sequence 3, Application US/09828000

; Patent No. 6596890

; GENERAL INFORMATION:

; APPLICANT: Government of the United States of America

; TITLE OF INVENTION: Vasostatin as Marrow Protectant

; FILE REFERENCE: 4239-55414

; CURRENT APPLICATION NUMBER: US/09/828,000

; CURRENT FILING DATE: 2001-04-06

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 3

; LENGTH: 180

; TYPE: PRT

; ORGANISM: Vasostatin

US-09-828-000-3

Query Match 100.0%; Score 327; DB 4; Length 180;

Best Local Similarity 100.0%; Pred. No. 9.9e-37;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 120 CGPCTKKVHVFYFNKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTVEVKIDNSQVESGSL 179
QY 61 E 61
DB 180 E 180

RESULT 3

US-09-828-000-2
; Sequence 2, Application US/09828000
; Patent No. 6596690
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/09/828,000
; CURRENT FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Calreticulin
US-09-828-000-2

Query Match 100.0%; Score 327; DB 4; Length 416;
Best Local Similarity 100.0%; Pred. No. 2.9e-36;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGPCTKKVHVFYFNKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTVEVKIDNSQVESGSL 60
DB 137 CGPCTKKVHVFYFNKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTVEVKIDNSQVESGSL 196
QY 61 E 61
DB 197 E 197

RESULT 4

US-09-828-000-4
; Sequence 4, Application US/09828000
; Patent No. 6596690
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/09/828,000
; CURRENT FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 4
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Fragment 1
US-09-828-000-4

Query Match 74.6%; Score 244; DB 4; Length 61;
Best Local Similarity 100.0%; Pred. No. 5e-26;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGPCTKKVHVFYFNKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTVEVKIDNSQVESGSL 44
DB 18 CGPCTKKVHVFYFNKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTVEVKIDNSQVESGSL 61

RESULT 5

US-09-828-000-7
; Sequence 7, Application US/09828000

; Patent No. 6596690
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/09/828,000
; CURRENT FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 7
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Fragment 4
US-09-828-000-7

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DB 1 VIFNKGKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTVEVKIDNSQVESGSL 35

RESULT 6

US-08-675-816-2
; Sequence 2, Application US/08675816
; Patent No. 6171864
; GENERAL INFORMATION:
; APPLICANT: Coughlan, Sean J.
; APPLICANT: Winfrey, Jr., Ron J.
; TITLE OF INVENTION: CALRETICULIN AND CALNEXIN GENES AND PROMOTER REGIONS AND USES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 701 Fifth Ave. Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/675,816
; FILING DATE: 05-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6171864tenburg, Carol
; REGISTRATION NUMBER: 39,317
; REFERENCE/DOCKET NUMBER: 750027.401
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206-622-4900
; TELEFAX: (206)-682-6031
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 415 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-675-816-2

Query Match 56.9%; Score 186; DB 3; Length 415;
Best Local Similarity 53.3%; Pred. No. 4.7e-17;
Matches 32; Conservative 11; Mismatches 17; Indels 0; Gaps 0;

QY 1 CGPCTKKVHVFYFNKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTVEVKIDNSQVESGSL 60
DB 138 CGVSTKKVHAILNYNDTNHLIKKEVPCETDQLTHVYTLIVRPDATYSILLIDNVEKQSGSL 197

RESULT 7
US-09-828-000-5
; Sequence 5, Application US/09828000
; Patent No. 6596690
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/09/828,000
; CURRENT FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 5
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Fragment 2
; US-09-828-000-5

Query Match 46.2%; Score 151; DB 4; Length 27;
Best Local Similarity 100.0%; Pred. No. 8.1e-14;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGPGTKKVVHVFYNYKGNVLINKDIRC 27
Db 1 CGPGTKKVVHVFYNYKGNVLINKDIRC 27

RESULT 8
US-08-296-362-2
; Sequence 2, Application US/08296362
; Patent No. 5691306
; GENERAL INFORMATION:
; APPLICANT: Bergeron, John J.M.
; APPLICANT: Thomas, David Y.
; APPLICANT: Wada, Ikuro
; TITLE OF INVENTION: METHODS OF DETECTION AND TREATMENT OF
; TITLE OF INVENTION: PROTEIN TRAFFICKING DISORDERS AND INCREASING SECRETORY
; TITLE OF INVENTION: PROTEIN PRODUCTION
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: SEED and BERRY
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/296,362
; FILING DATE: 25-AUG-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Deehr, Manya S.
; REGISTRATION NUMBER: 37,120
; REFERENCE/DOCKET NUMBER: 690066.401C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; TELEX: 3723836
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 593 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-296-362-2

Query Match 35.3%; Score 115.5; DB 1; Length 593;
Best Local Similarity 37.1%; Pred. No. 2.9e-07;

Matches 26; Conservative 12; Mismatches 21; Indels 11; Gaps 2;
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Db 195 CGE-DYKLHFIHRHKPKTGVFEKHAKRPDADUKTYFTDKKTHLYTLINPDSFELIV 253
Qy 51 DNSQVESGSL 60
Db 254 DQSVNSGNL 263

RESULT 9
US-09-976-594-947
; Sequence 947, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 947
; LENGTH: 610
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No. 6673549 3876162CD1
US-09-976-594-947

Query Match 32.9%; Score 107.5; DB 4; Length 610;
Best Local Similarity 35.7%; Pred. No. 3.8e-06;
Matches 25; Conservative 11; Mismatches 23; Indels 11; Gaps 2;

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Db 185 CGE-DYKLHFIHRHKPKTGVFEKHAKRPDVLKKKFTDRKTHLYTLVWNPDDTFELIV 243
Qy 51 DNSQVESGSL 60
Db 244 DQTVVNGSL 253

RESULT 10
US-09-828-000-6
; Sequence 6, Application US/09828000
; Patent No. 6596690
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/09/828,000
; CURRENT FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 6
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Fragment 3
; US-09-828-000-6

Query Match 29.4%; Score 96; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 VIFNYKGNVLINKDIRC 27
Db 1 VIFNYKGNVLINKDIRC 18

; APPLICANT: Liang, Jihong
; APPLICANT: Mittanck, Cindy A.
; APPLICANT: Seale, Jeffrey W.
; APPLICANT: Wu, Yonnie S.
; TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use
; FILE REFERENCE: 38-21(15036)B
; CURRENT APPLICATION NUMBER: US/09/732,210
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/169,513
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: US 60/169,340
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 1753
; SEQ ID NO 1163
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Porphyra purpurea
US-09-732-210-1163

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DB 10 PNKTEIALTYIYIGILSRSKELKKTINIDADIRQNLNDQQIVSIREIL---ESSYQI 66
QY 49 KIDNSQVESGSL 61
DB 67 EGDLEKRFESMSIK 79

RESULT 15
US-09-252-991A-18861
; Sequence 18861, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18861
; LENGTH: 588
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18861

Query Match 16.8%; Score 55; DB 4; Length 588;
Best Local Similarity 48.0%; Pred. No. 51;
Matches 12; Conservative 4; Mismatches 9; Indels 0; Gaps 0;
QY 15 KGNVLINKDIRKDDFTHTLYTLI 39
DB 364 RGDPLGKDIRKLDVDDVLYTAL 388

Search completed: October 4, 2004, 13:07:20
Job time : 14.6353 secs

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OM protein - protein search, using sw model

Run on: October 4, 2004, 13:06:03 ; Search time 44.8529 Seconds
(without alignments)
437.647 Million cell updates/sec

Title: US-09-807-148-5
Perfect score: 327
Sequence: 1 CGPGTKKHVIFNYKGNVL.....PONTVEYKIDNSQVESGSL 61

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1351062 segs, 321799191 residues

Total number of hits satisfying chosen parameters: 1351062

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
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- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
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- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	327	100.0	61	10	US-09-828-000-8
2	327	100.0	61	15	US-10-405-588-8
3	327	100.0	180	10	US-09-828-000-3
4	327	100.0	180	15	US-10-405-588-3
5	327	100.0	416	10	US-09-828-000-2
6	327	100.0	416	14	US-10-316-253-2
7	327	100.0	416	14	US-10-316-253-4
8	327	100.0	416	14	US-10-316-253-6
9	327	100.0	416	15	US-10-405-588-2
10	327	100.0	417	10	US-09-906-393A-36
11	327	100.0	417	14	US-10-161-959-29
12	327	100.0	417	15	US-10-367-093-14
13	244	74.6	61	10	US-09-828-000-4
14	244	74.6	61	15	US-10-405-588-4
15	219.5	67.1	395	15	US-10-369-493-6343
					Sequence 8, Appli
					Sequence 8, Appli
					Sequence 3, Appli
					Sequence 3, Appli
					Sequence 2, Appli
					Sequence 2, Appli
					Sequence 4, Appli
					Sequence 6, Appli
					Sequence 2, Appli
					Sequence 36, Appli
					Sequence 29, Appli
					Sequence 14, Appli
					Sequence 4, Appli
					Sequence 4, Appli

213 65.1 210 16 US-10-767-701-55877 Sequence 55877, A
189 57.8 35 10 US-09-828-000-7 Sequence 7, Appli
18 57.8 35 15 US-10-405-588-7 Sequence 7, Appli
19 188 57.5 346 12 US-10-425-114-48930 Sequence 48930, A
20 188 57.5 421 16 US-10-767-701-46544 Sequence 46544, A
21 188 57.5 435 12 US-10-425-114-70304 Sequence 70304, A
22 188 57.5 442 16 US-10-437-963-114914 Sequence 114914, A
23 188 57.5 667 16 US-10-437-963-114860 Sequence 114860, A
24 186 56.9 388 12 US-10-425-114-46405 Sequence 46405, A
25 186 56.9 391 12 US-10-425-114-69619 Sequence 69619, A
26 186 56.9 442 12 US-10-425-114-46869 Sequence 46869, A
27 185 56.6 290 12 US-10-425-114-44768 Sequence 44768, A
28 185 56.6 422 12 US-10-424-599-277445 Sequence 277445, A
29 184 56.3 390 15 US-10-161-927-46 Sequence 46, Appli
30 183 56.0 425 16 US-10-437-963-122222 Sequence 122222, A
31 180 55.0 391 12 US-10-424-599-190956 Sequence 190956, A
32 180 55.0 391 12 US-10-425-114-46328 Sequence 46328, A
33 180 55.0 420 12 US-10-424-599-190958 Sequence 190958, A
34 180 55.0 420 12 US-10-424-599-190958 Sequence 190958, A
35 180 55.0 424 16 US-10-437-963-201427 Sequence 201427, A
36 180 55.0 434 12 US-10-425-114-70140 Sequence 70140, A
37 180 55.0 439 12 US-10-425-114-65495 Sequence 65495, A
38 179 54.7 247 12 US-10-424-599-153809 Sequence 153809, A
39 179 54.7 372 12 US-10-425-114-44821 Sequence 44821, A
40 179 54.7 372 12 US-10-425-114-54997 Sequence 54997, A
41 179 54.7 418 12 US-10-424-599-153808 Sequence 153808, A
42 179 54.7 424 16 US-10-437-963-201420 Sequence 201420, A
43 175 53.5 279 16 US-10-767-701-39041 Sequence 39041, A
44 175 53.5 422 16 US-10-767-701-45264 Sequence 45264, A
45 175 53.5 431 16 US-10-767-701-44015 Sequence 44015, A

ALIGNMENTS

RESULT 1
US-09-828-000-8
; Sequence 8, Application US/09828000
; Publication No. US20030078198A1
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasoestat in as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/09/828,000
; CURRENT FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Fragment 5
US-09-828-000-8

Query Match 100.0%; Score 327; DB 10; Length 61;
Best Local Similarity 100.0%; Pred. No. 1.2e-35;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGPGTKKHVIFNYKGNVLINKDKCKDETHLYTLVRPONTVEYKIDNSQVESGSL 60
Db 1 CGPGTKKHVIFNYKGNVLINKDKCKDETHLYTLVRPONTVEYKIDNSQVESGSL 60
QY 61 E 61
Db 61 E 61

RESULT 2
US-10-405-588-8
; Sequence 8, Application US/10405588
; Publication No. US20030216299A1
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasoestat in as Marrow Protectant

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; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/10/405,588
; CURRENT FILING DATE: 2003-04-01
; PRIOR APPLICATION NUMBER: US/09/828,000
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Fragment 5
US-10-405-588-8

Query Match
Best Local Similarity 100.0%; Score 327; DB 15; Length 61;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 E 61
Db 61 E 61

RESULT 3
US-09-828-000-3
; Sequence 3, Application US/09828000
; Publication No. US20030078198A1
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/09/828,000
; CURRENT FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Vasostatin
US-09-828-000-3

Query Match
Best Local Similarity 100.0%; Score 327; DB 10; Length 180;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 E 61
Db 180 E 180

RESULT 4
US-10-405-588-3
; Sequence 3, Application US/10405588
; Publication No. US20030216299A1
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/10/405,588
; CURRENT FILING DATE: 2003-04-01
; PRIOR APPLICATION NUMBER: US/09/828,000
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-316-253-2

Query Match
Best Local Similarity 100.0%; Score 327; DB 14; Length 416;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 E 61
Db 197 E 197

RESULT 5
US-09-828-000-2
; Sequence 2, Application US/09828000
; Publication No. US20030078198A1
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/09/828,000
; CURRENT FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Calreticulin
US-09-828-000-2

Query Match
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Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 E 61
Db 197 E 197

RESULT 6
US-10-316-253-2
; Sequence 2, Application US/10316253
; Publication No. US20030162706A1
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Peters, Kevin
; APPLICANT: Thompson, Larry
; APPLICANT: Wang, Feng
; APPLICANT: Greis, Kenneth
; TITLE OF INVENTION: Angiogenesis Modulating Proteins
; FILE REFERENCE: 8865M
; CURRENT APPLICATION NUMBER: US/10/316,253
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: US 60/355,295
; PRIOR FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-316-253-2

Query Match
Best Local Similarity 100.0%; Score 327; DB 14; Length 416;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 137 CGPGTKKVHVIFNYKGNVLINKDIRCKDDEFTHLTYTLIVRPDNTYEVKIDNSQVESGSL 196
QY 61 E 61
Db 197 E 197
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Best Local Similarity 100.0%; Pred. No. 1.4e-34;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 61 E 61
DB 197 E 197

RESULT 7

US-10-316-253-4
; Sequence 4, Application US/10316253
; Publication No. US20030162706A1
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Peters, Kevin
; APPLICANT: Thompson, Larry
; APPLICANT: Wang, Feng
; APPLICANT: Greis, Kenneth
; TITLE OF INVENTION: Angiogenesis Modulating Proteins
; FILE REFERENCE: 8865M
; CURRENT APPLICATION NUMBER: US/10/316,253
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: US 60/355,295
; PRIOR FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-316-253-4

Query Match 100.0%; Score 327; DB 14; Length 416;
Best Local Similarity 100.0%; Pred. No. 1.4e-34;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 61 E 61
DB 197 E 197

RESULT 8

US-10-316-253-6
; Sequence 6, Application US/10316253
; Publication No. US20030162706A1
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Peters, Kevin
; APPLICANT: Thompson, Larry
; APPLICANT: Wang, Feng
; APPLICANT: Greis, Kenneth
; TITLE OF INVENTION: Angiogenesis Modulating Proteins
; FILE REFERENCE: 8865M
; CURRENT APPLICATION NUMBER: US/10/316,253
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: US 60/355,295
; PRIOR FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-316-253-6

Query Match 100.0%; Score 327; DB 14; Length 416;
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DB 197 E 197

RESULT 9

US-10-405-588-2
; Sequence 2, Application US/10405588
; Publication No. US20030216299A1
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/10/405,588
; CURRENT FILING DATE: 2003-04-01
; PRIOR APPLICATION NUMBER: US/09/828,000
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Calreticulin
US-10-405-588-2

Query Match 100.0%; Score 327; DB 15; Length 416;
Best Local Similarity 100.0%; Pred. No. 1.4e-34;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 61 E 61
DB 197 E 197

RESULT 10

US-09-906-393A-36
; Sequence 36, Application US/09906393A
; Publication No. US20030039970A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Zhou
; APPLICANT: Xiao, Wuhan
; TITLE OF INVENTION: METHOD OF PROGNOSING CANCER AND THE PROTEINS INVOLVED
; FILE REFERENCE: 1720-1-001CIP
; CURRENT APPLICATION NUMBER: US/09/906,393A
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/218,761
; PRIOR FILING DATE: 2000-07-17
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-906-393A-36

Query Match 100.0%; Score 327; DB 10; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.4e-34;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGPGTKKHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSL 60

Db 137 CGPGTKKVHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSL 196

Qy 61 E 61

Db 197 E 197

RESULT 11

US-10-161-959-29
; Sequence 29, Application US/10161959
; Publication No. US2003009674A1
; GENERAL INFORMATION:
; APPLICANT: Holoshitz, Joseph
; APPLICANT: Ling, Song
; TITLE OF INVENTION: Methods and Compositions for the Treatment of Diseases Associated
; FILE REFERENCE: UM-07135
; CURRENT APPLICATION NUMBER: US/10/161,959
; PRIOR FILING DATE: 2002-10-01
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-161-959-29

Query Match 100.0%; Score 327; DB 14; Length 417;

Best Local Similarity 100.0%; Pred. No. 1.4e-34;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGPGTKKVHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSL 60

Db 137 CGPGTKKVHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSL 196

Qy 61 E 61

Db 197 E 197

RESULT 12

US-10-367-093-14
; Sequence 14, Application US/10367093
; Publication No. US20030216315A1
; GENERAL INFORMATION:
; APPLICANT: Duke University
; APPLICANT: Nicchitta, Chris
; APPLICANT: Baker-LePain, Julie
; TITLE OF INVENTION: MODULATION OF IMMUNE RESPONSE BY NON-PEPTIDE BINDING STRESS RESPO
; FILE REFERENCE: 180/145
; CURRENT APPLICATION NUMBER: US/10/367,093
; CURRENT FILING DATE: 2003-02-13
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-367-093-14

Query Match 100.0%; Score 327; DB 15; Length 417;

Best Local Similarity 100.0%; Pred. No. 1.4e-34;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGPGTKKVHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSL 60

Db 137 CGPGTKKVHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSL 196

Qy 61 E 61

Db 197 E 197

RESULT 13

US-09-828-000-4
; Sequence 4, Application US/09828000
; Publication No. US20030078198A1
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/09/828,000
; CURRENT FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Fragment 1
US-09-828-000-4

Query Match 74.6%; Score 244; DB 10; Length 61;

Best Local Similarity 100.0%; Pred. No. 1.2e-24;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGPGTKKVHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPD 44

Db 18 CGPGTKKVHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPD 61

RESULT 14

US-10-405-588-4
; Sequence 4, Application US/10405588
; Publication No. US20030216299A1
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/10/405,588
; CURRENT FILING DATE: 2003-04-01
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Fragment 1
US-10-405-588-4

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Best Local Similarity 100.0%; Pred. No. 1.2e-24;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGPGTKKVHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPD 44

Db 18 CGPGTKKVHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPD 61

RESULT 15

US-10-369-493-6343
; Sequence 6343, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cac, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

Mon Oct 4 14:24:05 2004

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; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 6343
; LENGTH: 395
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-6343

Query Match      67.1%; Score 219.5; DB 15; Length 395;
Best Local Similarity 67.2%; Pred. No. 2.4e-20;
Matches 41; Conservative 7; Mismatches 12; Indels 1; Gaps 1;

QY      1 CGPGTKKHVITFNKGNVLINKDIRCKDDEFTHLTVLRPDNTYEYKIDNSQVESGSL 60
Db      133 CGP-TRRVHVILNKGKNIKKKEITCKSDDELTHLYTLILNSDNTYEYKIDGESACTGSL 191

QY      61 E 61
Db      192 E 192
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Search completed: October 4, 2004, 13:17:33
Job time : 45.8529 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 4, 2004, 12:55:52 ; Search time 13.2765 Seconds
(without alignments)
441.961 Million cell updates/sec

Title: US-09-807-148-5

Perfect score: 327
Sequence: 1 CGPGTKKHVIFNYKGNVL.....PDNTYEVKIDNSQVESGSL 61

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: PIR_78:*

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	327	100.0	416	1 S06763	calreticulin precu
2	327	100.0	416	2 JH0819	calreticulin precu
3	327	100.0	417	1 A37047	calreticulin precu
4	327	100.0	418	1 A34154	calreticulin precu
5	322	98.5	400	2 A34376	calreticulin, brai
6	322	98.5	421	2 S63799	calreticulin precu
7	280	88.7	405	1 JH0795	calreticulin precu
8	287	87.8	384	2 S29130	calreticulin (clon
9	287	87.8	411	2 S29129	calreticulin precu
10	278	85.0	406	2 A56637	calreticulin homol
11	271	82.9	419	2 S71343	calreticulin precu
12	251	76.8	336	2 A32507	41K larval antigen
13	236	72.2	393	1 A48573	calreticulin autoa
14	219.5	67.1	395	2 S25851	calreticulin precu
15	193	59.0	416	2 T4554	calreticulin - bee
16	188	57.5	421	2 S58170	calreticulin precu
17	186	56.9	415	2 T0172	calreticulin - cas
18	185	56.6	412	2 T05703	calreticulin - bar
19	185	56.6	415	2 C96605	calreticulin (Crt1
20	181	55.4	425	2 C96605	calreticulin - com
21	178	54.4	389	2 T03691	calreticulin call
22	178	54.4	416	2 T03698	calreticulin call
23	178	54.4	444	2 H86224	hypothetical prote
24	177	54.1	422	2 T07841	probable calreticu
25	117.5	35.9	592	2 I53260	calnexin - human
26	117.5	35.9	592	2 A46673	calnexin precursor
27	116.5	35.6	591	2 B54354	calnexin precursor
28	116.5	35.6	591	2 C54354	calnexin precursor
29	115.5	35.3	593	1 A37273	calnexin precursor

30	114.5	35.0	582	2 A46637	calnexin homolog S
31	109.5	33.5	622	2 S71342	calnexin precursor
32	106.5	32.6	611	2 A53418	calnexin precursor
33	106.5	32.6	611	2 A54086	calnexin-t - mouse
34	101.5	31.0	619	2 S40938	hypothetical prote
35	99	30.3	560	2 S56142	calcium-binding pr
36	90.5	27.7	546	2 T06415	calnexin - soybean
37	88.5	27.1	297	2 S70552	calnexin homolog C
38	85.5	26.1	530	2 JN0597	calnexin-like prot
39	84	25.7	356	2 A46164	calnexin - human
40	80.5	24.6	540	2 T10892	probable calnexin
41	78.5	24.0	428	2 T03251	calnexin - maize
42	75.5	23.1	532	2 T49873	calnexin homolog -
43	73.5	22.5	540	1 JU0470	site-specific DNA-
44	64.5	19.7	981	2 T46330	hypothetical prote
45	64	19.6	451	2 T16162	hypothetical prote

ALIGNMENTS

RESULT 1

S06763
calreticulin precursor - mouse
N:Alternate names: S5K calcium-binding reticuloplasmin; calregulin
C:Species: Mus musculus (house mouse)
C>Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S06763; JCI1444; FCI1233; AS7498
R:Smith, M.J.; Koch, G.L.E.
EMBO J. 8, 3581-3586, 1989
A>Title: Multiple zones in the sequence of calreticulin (CRP55, calregulin, HACBP), a m
A:Reference number: S06763; MUID:90C59955; PMID:2583110
A:Accession: S06763
A:Molecule type: DNA
A:Residues: 1-416 <SML>
A:Cross-references: ENBL:X14926; NID:G50567; PIDN:CAA33053.1; PID:G50568
R:Mazzarella, R.A.; Gold, P.; Cunningham, M.; Green, M.
Gene 120, 217-225, 1992
A>Title: Determination of the sequence of an expressible cDNA clone encoding ERp60/calr
A:Reference number: JCI1444; MUID:93C13037; PMID:1398135
A:Accession: JCI1444
A:Molecule type: mRNA
A:Residues: 1-416 <MAZ>
A:Cross-references: GB:M92988; NID:G193084; PIDN:AAA37569.1; PID:G193085
A:Accession: PC1233
A:Molecule type: protein
A:Residues: 18-41 <MA2>
R:White, T.K.; Zhu, Q.; Tanzer, M.L.
J. Biol. Chem. 270, 15928-15929, 1995
A>Title: Cell surface calreticulin is a putative mannoside lectin which triggers mouse
A:Reference number: AS7498; MUID:95332280; PMID:7608143
A:Accession: AS7498
A>Status: preliminary
A:Molecule type: protein
A:Residues: 74-80;142-151;186-193 <WHI>
C:Superfamily: calreticulin
C:Keywords: calcium binding
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-416/Product: calregulin #status experimental <MAI>
F:413-416/Region: endoplasmic reticulum retention signal

Query Match 100.0%; Score 327; DB 1; Length 416;
Best Local Similarity 100.0%; Pred. No. 1.4e-30;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	CGPGTKKHVIFNYKGNVLINKDICKDEFFHLYIVRPNTYEVKIDNSQVESGSL	60
DB	137	CGPGTKKHVIFNYKGNVLINKDICKDEFFHLYIVRPNTYEVKIDNSQVESGSL	196
QY		61 E 61	
DB		197 E 197	

RESULT 2

JH0819
 A;Title: calreticulin precursor - rat
 N;Alternate names: calcium-binding protein 3
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 20-Jun-2000
 C;Accession: JH0819; A49176; S11205; PCL109; S45036; S04867; S39372; A34473; S13045
 R;Nakamura, M.; Moriya, M.; Baba, T.; Michikawa, Y.; Yamanobe, T.; Arai, K.; Okinaga, S.
 Exp. Cell Res. 205, 101-110, 1993
 A;Title: An endoplasmic reticulum protein, calreticulin, is transported into the acrosome
 A;Reference number: A49176; MUID:93202172; PMID:8453984
 A;Accession: JH0819
 A;Molecule type: mRNA
 A;Residues: 1-416 <NAK>
 A;Cross-references: GB:D78308; NID:G1089798; PIDN:BAAL11345.1; PID:G1845572
 A;Accession: A49176
 A;Status: preliminary
 A;Molecule type: mRNA; protein
 A;Residues: 1-416 <NA2>
 A;Cross-references: GB:D78308; NID:G1089798; PIDN:BAAL11345.1; PID:G1845572
 A;Experimental source: Sprague-Dawley, spermatogenic cells
 A;Note: sequence extracted from NCBI backbone (NCBIN:127639, NCBIIP:127643)
 R;Murthy, K.K.; Banville, D.; Srikanth, C.B.; Carrier, F.; Holmes, C.; Bell, A.; Patel, Y.
 Nucleic Acids Res. 18, 4933, 1990
 A;Title: Structural homology between the rat calreticulin gene product and the Onchocerca
 A;Reference number: S11205; MUID:90370496; PMID:2395861
 A;Accession: S11205
 A;Molecule type: mRNA
 A;Residues: 1-416 <MUR>
 A;Cross-references: EMBL:X53363; NID:G55854; PIDN:CAA37446.1; PID:G55855
 R;Nakamura, M.; Michikawa, Y.; Baba, T.; Okinaga, S.; Arai, K.
 Biochem. Biophys. Res. Commun. 166, 668-673, 1992
 A;Title: Calreticulin is present in the acrosome of spermatozoa of rat testis.
 A;Reference number: PCL109; MUID:92360010; PMID:1497655
 A;Accession: PCL109
 A;Molecule type: protein
 A;Residues: 18-32 <NAK2>
 A;Experimental source: testis, strain Sprague-Dawley
 R;Soennichsen, B.; Fueflekrug, J.; van Nguyen, P.; Diekmann, W.; Robinson, D.G.; Mieskes
 submitted to the EMBL Data Library, May 1994
 A;Description: Retention and retrieval: both mechanisms cooperate to maintain calreticulin
 A;Reference number: S45036
 A;Accession: S45036
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-416 <SOE>
 A;Cross-references: EMBL:X79327; NID:G488840; PIDN:CAA55890.1; PID:G488841
 R;Lone, Y.C.; Bailly, A.; Latruffe, N.
 submitted to the EMBL Data Library, December 1989
 A;Reference number: S04867
 A;Accession: S04867
 A;Molecule type: protein
 A;Residues: 'R', 270-358, 'AAG', 'LON' <LON>
 A;Cross-references: EMBL:X13702; NID:G56055; PIDN:CAA31987.1; PID:G930260
 A;Note: the authors designated the protein as D-beta-hydroxybutyrate dehydrogenase
 R;Yokoi, T.; Nagayama, S.; Kajiwara, R.; Kawaguchi, Y.; Horiuchi, R.; Kamataki, T.
 Biochim. Biophys. Acta 1158, 339-344, 1993
 A;Title: Identification of protein disulfide isomerase and calreticulin as autoimmure an
 A;Reference number: S39371; MUID:94072621; PMID:8251535
 A;Accession: S39372
 A;Molecule type: protein
 A;Residues: 18-23 'X', 25-32 <YOK>
 R;Van, P.N.; Peter, F.; Seeling, H.D.
 J. Biol. Chem. 264, 17494-17501, 1989
 A;Title: Four intracisternal calcium-binding glycoproteins from rat liver microsomes with
 itive calcium sequestering rat liver vesicles.
 A;Reference number: A34473; MUID:90008920; PMID:2793869
 A;Accession: A34473
 A;Status: preliminary
 A;Molecule type: Protein
 A;Residues: 18-36 <VAN>
 R;Rieves, S.; de Mattei, M.; Lanfredi, M.; Villa, A.; Green, N.M.; MacLennan, D.H.; Meld

Biochem. J. 271, 473-480, 1990
 A;Title: Calreticulin is a candidate for a calsequestrin-like function in Ca(2+)-storage
 A;Reference number: S13045; MUID:91054414; PMID:2241926
 A;Accession: S13045
 A;Molecule type: protein
 A;Residues: 18-29 <TRE>
 C;Superfamily: calreticulin
 C;Keywords: calcium binding; glycoprotein
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 F;18-416/Product: calreticulin #status experimental <MAT>
 F;204-212/Region: nuclear location signal
 F;413-416/Region: endoplasmic reticulum retention signal
 F;344/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 100.0%; Score 327; DB 2; Length 416;
 Best Local Similarity 100.0%; Pred. NO. 1.4e-30;
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGPQTKVHVFYKGNVLINLKDIRCKDDEFTHTLYTLIVRPDNTYEKIDNSQVSGSL 60
 DB 137 CGPQTKVHVFYKGNVLINLKDIRCKDDEFTHTLYTLIVRPDNTYEKIDNSQVSGSL 196
 QY 61 E 61
 DB 197 E 197
 RESULT 3
 A37047
 calreticulin precursor - human
 N;Alternate names: 52K ribonucleoprotein autoantigen Ro/SS-A; 60K integrin-binding prote
 C;Species: Homo sapiens (man)
 C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 18-Feb-2000
 C;Accession: A42330; A37047; A46452; A28812; PH1525; A40346; S11475; T45075
 R;McCaulliffe, D.P.; Yang, Y.S.; Wilson, J.; Sontheimer, R.D.; Capra, J.D.
 J. Biol. Chem. 267, 2557-2562, 1992
 A;Title: The 5'-flanking region of the human calreticulin gene shares homology with the
 A;Reference number: A42330; MUID:92129342; PMID:1733953
 A;Accession: A42330
 A;Molecule type: DNA
 A;Residues: 1-417 <MC2>
 A;Note: sequence extracted from NCBI backbone (NCBIN:78537, NCBIIP:78536)
 R;McCaulliffe, D.P.; Lux, F.A.; Lieu, T.S.; Sanz, I.; Hanke, J.; Newkirk, M.M.; Bachinski
 J. Clin. Invest. 85, 1379-1391, 1990
 A;Title: Molecular cloning, expression, and chromosome 19 localization of a human Ro/SS-
 A;Reference number: A37047; MUID:90237213; PMID:2332496
 A;Accession: A37047
 A;Molecule type: mRNA
 A;Residues: 1-417 <MCC>
 A;Cross-references: GB:M32294; NID:G337486; PIDN:AAA36592.1; PID:G337487
 A;Note: the authors translated the codon GTA for residue 349 as Tyr
 R;Rokeach, J.A.; Haselby, J.A.; Mellof, J.F.; Smeenk, R.J.; Unnasch, T.R.; Greene, B.M.;
 J. Immunol. 147, 3031-3039, 1991
 A;Title: Characterization of the autoantigen calreticulin.
 A;Reference number: A46452; MUID:92013129; PMID:1919005
 A;Accession: A46452
 A;Molecule type: mRNA
 A;Residues: 1-417 <ROK>
 A;Cross-references: GB:M84739; NID:G179881; PIDN:AAA51916.1; PID:G179882
 A;Note: sequence extracted from NCBI backbone (NCBIN:60749, NCBIIP:60750)
 R;Lieu, T.S.; Newkirk, M.M.; Capra, J.D.; Sontheimer, R.D.
 J. Clin. Invest. 82, 96-101, 1988
 A;Title: Molecular characterization of human Ro/SS-A antigen. Amino terminal sequence of
 A;Reference number: A28812; MUID:88273610; PMID:3260607
 A;Accession: A28812
 A;Molecule type: protein
 A;Residues: 18-41 <LIE>
 A;Note: 18-Ala was also found
 R;Dupuis, M.; Schaefer, E.; Krause, K.H.; Tschopp, J.
 J. Exp. Med. 177, 1-7, 1993
 A;Title: The calcium-binding protein calreticulin is a major constituent of lytic granul
 A;Reference number: PH1525; MUID:93115648; PMID:8418194
 A;Accession: PH1525

A:Molecule type: protein
 A:Residues: 18-27 <DUP>
 A:Experimental source: LAK cell
 A:Superfamily: calreticulin
 C:Keywords: skeletal muscle
 Biochemistry 30, 9859-9866, 1991
 A:Title: In vitro interaction of a polypeptide homologous to human Ro/SS-A antigen (calreticulin) with a Ca(2+)-binding protein that co-purifies with calreticulin from skeletal muscle
 A:Reference number: A40346; MUID:92002034; PMID:1911778
 A:Accession: A40346
 A:Molecule type: protein
 A:Residues: 18-34, R' <ROU>
 R:Krause, K.H.; Simmerman, H.K.B.; Jones, L.R.; Campbell, K.P.
 Biochem. J. 270, 545-548, 1990
 A:Title: Sequence similarity of calreticulin with a Ca(2+)-binding protein that co-purifies with calreticulin from skeletal muscle
 A:Reference number: S11475; MUID:90380058; PMID:2400400
 A:Accession: S11475
 A:Molecule type: protein
 A:Residues: 18-32 <KRA>
 R:Damerdin, J.; McCreedy, P.; Stillwagen, S.; Ramirez, M.; Carrano, A.
 submitted to the EMBL Data Library, November 1996
 A:Description: Characterization by genomic sequence analysis of a gene-rich 111 kb region containing the calreticulin gene
 A:Reference number: Z22906
 A:Accession: T45075
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-417 <LAM>
 A:Cross-references: EMBL:AD000092; PIDN:AB51176.1
 A:Experimental source: cell line SHL2-B; fibroblast
 C:Comment: Autoantibodies specific for this protein are found in Sjogren's syndrome and Sjogren's syndrome-like syndrome
 C:Genetics:
 A:Gene: GDB:CALR
 A:Cross-references: GDB:125179; OMIM:109091
 A:Map position: 19p13.3-19p13.2
 A:Introns: 31/1; 65/1; 133/1; 164/3; 234/3; 320/3; 351/3
 A:Note: CRT
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 C:Keywords: calcium binding; integrin binding
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 F:414-417/Region: endoplasmic reticulum retention signal

Query Match 100.0%; Score 327; DB 1; Length 417;
 Best Local Similarity 100.0%; Pred. No. 1.4e-30;
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGPGTKKVHVIFNYKGNVLINKDIRCKDDEFTHTLYTLVRPNTYEVKIDNSQVESGSL 60
 Db 137 CGPGTKKVHVIFNYKGNVLINKDIRCKDDEFTHTLYTLVRPNTYEVKIDNSQVESGSL 196

QY 61 E 61
 Db 197 E 197

RESULT 4
 A34154
 Calreticulin precursor, skeletal muscle - rabbit
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: A34154; S13047
 R:Fliegel, L.; Burns, K.; MacLennan, D.H.; Reithmeier, R.A.F.; Michalak, M.
 J. Biol. Chem. 264, 21522-21528, 1989
 A:Title: Molecular cloning of the high affinity calcium-binding protein (calreticulin) cDNA from rabbit skeletal muscle
 A:Reference number: A34154; MUID:90094320; PMID:2600080
 A:Accession: A34154
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-418 <FLI>
 A:Cross-references: GB:J05138; NID:G164859; PIDN:AAA31188.1; PID:G164859
 R:Treves, S.; de Mattei, M.; Lanfredi, M.; Villa, A.; Green, N.M.; MacLennan, D.H.; Meldolesi, J. 271, 473-480, 1990
 Biochem. J. 271, 473-480, 1990
 A:Title: Calreticulin is a candidate for a calsequestrin-like function in Ca(2+)-storage organelles
 A:Reference number: S13045; MUID:910504414; PMID:2241926
 A:Accession: S13047

A:Molecule type: protein
 A:Residues: 19-32 <TRE>
 C:Superfamily: calreticulin
 C:Keywords: skeletal muscle
 F:1-17/Domain: signal sequence #status predicted <SIG>
 F:415-418/Region: endoplasmic reticulum retention signal

Query Match 100.0%; Score 327; DB 1; Length 418;
 Best Local Similarity 100.0%; Pred. No. 1.4e-30;
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGPGTKKVHVIFNYKGNVLINKDIRCKDDEFTHTLYTLVRPNTYEVKIDNSQVESGSL 60
 Db 137 CGPGTKKVHVIFNYKGNVLINKDIRCKDDEFTHTLYTLVRPNTYEVKIDNSQVESGSL 196

QY 61 E 61
 Db 197 E 197

RESULT 5
 S43376
 Calreticulin, brain isoform 1 - bovine
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 20-Oct-1994 #sequence_revision 23-Mar-1995 #text_change 07-May-1999
 C:Accession: S43376; S36801
 R:Matsuoka, K.; Seta, K.; Yamakawa, Y.; Okuyama, T.; Shinoda, T.; Isobe, T.
 Biochem. J. 298, 435-442, 1994
 A:Title: Covalent structure of bovine brain calreticulin.
 A:Reference number: S43376; MUID:94183174; PMID:8135753
 A:Accession: S43376
 A:Molecule type: protein
 A:Residues: 1-400 <MAT>
 A:Experimental source: Brain
 R:Li, N.; Fine, R.E.; Johnson, R.J.
 Biochim. Biophys. Acta 1202, 70-76, 1993
 A:Title: Comparison of cDNAs from bovine brain coding for two isoforms of calreticulin
 A:Reference number: S36799; MUID:93385184; PMID:8373827
 A:Accession: S36801
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 45-63, E', 65-83 <LIU>
 A:Experimental source: Brain, clone 8.1
 C:Superfamily: calreticulin
 C:Keywords: calcium binding; glycoprotein
 F:397-400/Region: endoplasmic reticulum retention signal
 F:120-146/Dissulfide bonds: #status experimental
 F:162/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 98.5%; Score 322; DB 2; Length 400;
 Best Local Similarity 98.4%; Pred. No. 5.3e-40;
 Matches 60; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGPGTKKVHVIFNYKGNVLINKDIRCKDDEFTHTLYTLVRPNTYEVKIDNSQVESGSL 60
 Db 120 CGPGTKKVHVIFNYKGNVLINKDIRCKDDEFTHTLYTLVRPNTYEVKIDNSQVESGSL 179

QY 61 E 61
 Db 180 E 180

RESULT 6
 S36799
 Calreticulin precursor, brain isoform 2 - bovine
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 10-Dec-1993 #sequence_revision 23-Mar-1995 #text_change 13-Aug-1999
 C:Accession: S36799; S36800
 R:Li, N.; Fine, R.E.; Johnson, R.J.
 Biochim. Biophys. Acta 1202, 70-76, 1993
 A:Title: Comparison of cDNAs from bovine brain coding for two isoforms of calreticulin
 A:Reference number: S36799; MUID:93385184; PMID:8373827
 A:Accession: S36799

A:Molecule type: mRNA
 A:Residues: 1-421 <LIU>
 A:Cross-references: GB:L13452; NID:G348693; PIDN:AAC37307.1; PID:G348694
 A:Experimental source: brain, clone 9.4
 A:Accession: S36800
 A:Molecule type: protein
 A:Residues: 35-45 <L12>
 C:Superfamily: calreticulin
 C:Keywords: calcium binding; glycoprotein
 F:1-34/Domain: signal sequence #status predicted <SIG>
 F:35-421/Product: calreticulin, brain isoform 2 #status predicted <MAT>
 F:418-421/Region: endoplasmic reticulum retention signal
 F:141-167/Disulfide bonds: #status predicted
 F:183/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 98.5%; Score 322; DB 2; Length 421;
 Best Local Similarity 98.4%; Pred. No. 5.6e-30; Indels 0; Gaps 0;
 Matches 60; Conservative 1; Mismatches 0

QY 1 CGPGTKKVVHVFNYKGNVINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSL 60
 DB 141 CGPGTKKVVHVFNYKGNVINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSL 200

QY 61 E 61
 DB 201 E 201

RESULT 7
 JH0795
 calreticulin precursor - California sea hare
 N:Alternate names: protein 407
 C:Species: Aplysia californica (California sea hare)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: JH0795; B31409; F60977
 R:Kennedy, T.E.; Kuhl, D.; Barzilai, A.; Sweatt, J.D.; Kandel, E.R.
 Neuron 9, 1013-1024, 1992
 A:Title: Long-term sensitization training in aplysia leads to an increase in calreticulin
 A:Reference number: JH0795; MUID:93098937; PMID:1463604
 A:Accession: JH0795
 A:Molecule type: mRNA
 A:Residues: 1-405 <KEN>
 A:Cross-references: GB:S51239; NID:G262053; PIDN:AAB24569.1; PID:G262054
 A:Experimental source: abdominal ganglion and antral nervous system
 R:Kennedy, T.E.; Gawinowicz, M.A.; Barzilai, A.; Kandel, E.R.; Sweatt, J.D.
 Proc. Natl. Acad. Sci. U.S.A. 85, 7008-7012, 1988
 A:Title: Sequencing of proteins from two-dimensional gels by using in situ digestion and
 tion in Aplysia.
 A:Reference number: A94207; MUID:88320566; PMID:3413132
 A:Accession: B31409
 A:Molecule type: protein
 A:Residues: 'X', 17-28, 'X', 30-31 <XE2>
 R:Sweatt, J.D.; Kennedy, T.E.; Wager-Smith, K.; Gawinowicz, M.A.; Barzilai, A.; Karl, K.
 Electrophoresis 10, 152-157, 1989
 A:Title: Development of a database of amino acid sequences for proteins identified and i
 A:Reference number: A60977; MUID:89276264; PMID:2731514
 A:Accession: F60977
 A:Molecule type: protein
 A:Residues: 'X', 17-28, 'X', 30-31 <SWE>
 C:Superfamily: calreticulin
 C:Keywords: calcium binding; endoplasmic reticulum
 F:1-15/Domain: signal sequence #status predicted <SIG>
 F:16-405/Product: calreticulin #status predicted <MAT>
 F:402-405/Region: endoplasmic reticulum retention signal

Query Match 88.7%; Score 290; DB 1; Length 405;
 Best Local Similarity 85.2%; Pred. No. 3e-26; Indels 5; Gaps 0;
 Matches 52; Conservative 4; Mismatches 5

QY 1 CGPGTKKVVHVFNYKGNVINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSL 60
 DB 133 CGPGTKKVVHVFNYKGNVINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSL 192

QY 61 E 61
 DB 193 E 193

RESULT 8
 S29130
 calreticulin (clone 8) - African clawed frog (fragment)
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
 C:Accession: S29130; T01068
 R:Treves, S.; Zorzato, F.; Pozzan, T.
 Biochem. J. 287, 579-581, 1992
 A:Title: Identification of calreticulin isoforms in the central nervous system.
 A:Reference number: S29129; MUID:93074997; PMID:1445218
 A:Accession: S29130
 A:Molecule type: mRNA
 A:Residues: 1-384 <PRE>
 A:Cross-references: EMBL:X67598
 A:Accession: T01068
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-339, 'XTGR' <TRW>
 A:Cross-references: EMBL:X67598; NID:G64610; PIDN:CAA47867.1; PID:G64611
 A:Experimental source: CNS
 C:Superfamily: calreticulin
 C:Keywords: glycoprotein
 F:381-384/Region: endoplasmic reticulum retention signal
 F:316/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 87.8%; Score 287; DB 2; Length 384;
 Best Local Similarity 88.5%; Pred. No. 6.4e-26;
 Matches 54; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 CGPGTKKVVHVFNYKGNVINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSL 60
 DB 109 CGPGTKKVVHVFNYKGNVINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSL 168

QY 61 E 61
 DB 169 E 169

RESULT 9
 S29129
 calreticulin precursor (clone 3) - African clawed frog (fragment)
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
 C:Accession: S29129
 R:Treves, S.; Zorzato, F.; Pozzan, T.
 Biochem. J. 287, 579-581, 1992
 A:Title: Identification of calreticulin isoforms in the central nervous system.
 A:Reference number: S29129; MUID:93074997; PMID:1445218
 A:Accession: S29129
 A:Molecule type: mRNA
 A:Residues: 1-411 <TRB>
 A:Cross-references: EMBL:X67597; NID:G64608; PIDN:CAA47866.1; PID:G64609
 C:Superfamily: calreticulin
 C:Keywords: glycoprotein
 F:1-12/Domain: signal sequence (fragment) #status predicted <SIG>
 F:13-411/Product: calreticulin #status predicted <MAT>
 F:408-411/Region: endoplasmic reticulum retention signal
 F:339/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 87.8%; Score 287; DB 2; Length 411;
 Best Local Similarity 88.5%; Pred. No. 6.9e-26;
 Matches 54; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 CGPGTKKVVHVFNYKGNVINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSL 60
 DB 132 CGPGTKKVVHVFNYKGNVINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSL 191

QY 61 E 61

```
Db 192 E 192
Query Match 82.9%; Score 271; DB 2; Length 419;
Best Local Similarity 83.6%; Pred. No. 5.3e-24;
Matches 51; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

RESULT 10
A56637
calreticulin homolog precursor - fruit fly (Drosophila melanogaster)
N:Alternate names: Ro/SS-A autoantigen/calreticulin homolog
C:Species: Drosophila melanogaster
C>Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 13-Aug-1999
C:Accession: A56637; A37158
R:Smith, M.J.
DNA Seq. 3, 247-250, 1992
A:Title: Nucleotide sequence of a Drosophila melanogaster gene encoding a calreticulin h
A:Reference number: A56637; MUID:93208374; PMID:1296819
A:Accession: A56637
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-406 <SMI>
A:Cross-references: GB:X64461; NID:G7685; PIDN:CAA45791.1; PID:G7686
A>Note: sequence extracted from NCBI backbone (NCBIN:128274, NCBIP:128275)
R:McCaulliffe, D.P.; Zappi, E.; Lieu, T.S.; Michalak, M.; Sontheimer, R.D.; Capra, J.D.
J. Clin. Invest. 86, 332-335, 1990
A:Title: A human Ro/SS-A autoantigen is the homologue of calreticulin and is highly hom
A:Reference number: A37158; MUID:90307981; PMID:2385822
A:Accession: A37158
A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: DNA
A:Residues: 91-105,'A',107,109-124,182-183,'L',185-220 <MCC>
C:Genetics:
A:Gene: FlyBase:Crc
A:Cross-references: FlyBase:FBgn0005585
A:Introns: 65/1; 222/3
C:Superfamily: calreticulin
C:Keywords: calcium binding; endoplasmic reticulum
F:1-17/Domain: signal sequence #status predicted <SIG>
F:403-406/Region: endoplasmic reticulum retention signal

Query Match 85.0%; Score 278; DB 2; Length 406;
Best Local Similarity 83.6%; Pred. No. 7.7e-25;
Matches 51; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 CGPGTKKVHVIFNYKGNVLINCKDIRCKDDFTHLYTLIVRPNTYEVKIDNSQVSGSL 60
DB 137 CGPGTKKVHVIFSYKGNHLISKDIRCKDDVTHFYTLIVRPNTYEVLDNEKVESGSL 196
QY 61 E 61
DB 197 E 197

RESULT 11
S71343
calreticulin precursor - Korean frog
C:Species: Rana rugosa (Korean frog)
C>Date: 29-Jan-1998 #sequence_revision 13-Feb-1998 #text_change 20-Jun-2000
C:Accession: S71343
R:Yamamoto, S.; Nakamura, M.
FEBS Lett. 387, 27-32, 1996
A:Title: Calnexin: its molecular cloning and expression in the liver of the frog, Rana
A:Reference number: S71342; MUID:96234004; PMID:8654561
A:Accession: S71343
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-419 <YAM>
A:Cross-references: EMBL:D78589; NID:g1514956; PIDN:BAAL1425.1; PID:g1514957
C:Superfamily: calreticulin
C:Keywords: calcium binding; endoplasmic reticulum
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-419/Product: calreticulin #status predicted <YAT>
F:205-213/Region: nuclear location signal
F:415-418/Region: endoplasmic reticulum retention signal

Query Match 72.2%; Score 236; DB 1; Length 393;
Best Local Similarity 73.8%; Pred. No. 6.2e-20;
Matches 45; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 CGPGTKKVHVIFNYKGNVLINCKDIRCKDDFTHLYTLIVRPNTYEVKIDNSQVSGSL 60
DB 135 CGMATKKVHVIFNYKGNHLIKKIPCKDDLKTHLYTLIVPNPNKYEVLDNAKVESGSL 194
QY 61 E 61
DB 195 E 195

Query Match 76.8%; Score 251; DB 2; Length 336;
Best Local Similarity 75.4%; Pred. No. 9.2e-22;
Matches 46; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 1 CGPGTKKVHVIFNYKGNVLINCKDIRCKDDFTHLYTLIVRPNTYEVKIDNSQVSGSL 60
DB 83 CGPGTKKVHVIFHYKDRNMHKDIRCKDDVTHFYTLIVNSDNTYEVQIDGKAESGEL 142
QY 61 E 61
DB 143 E 143

RESULT 13
A48573
calreticulin autoantigen homolog precursor - fluke (Schistosoma mansoni)
C:Species: Schistosoma mansoni
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A48573
R:Khaliq, J.; Trottein, F.; Schacht, A.M.; Godin, C.; Pierce, R.J.; Capron, A.
Mol. Biochem. Parasitol. 57, 193-202, 1993
A:Title: Cloning of the gene encoding a Schistosoma mansoni antigen homologous to human
A:Reference number: A48573; MUID:93165070; PMID:8433712
A:Accession: A48573
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-393 <KHA>
A:Cross-references: GB:M93097; NID:g160928
A>Note: sequence inconsistent with the nucleotide translation
A>Note: sequence extracted from NCBI backbone (NCBIN:125085, NCBIP:125086)
C:Superfamily: calreticulin
F:1-16/Domain: signal sequence #status predicted <SIG>
F:390-393/Region: endoplasmic reticulum retention signal

Query Match 77.2%; Score 236; DB 1; Length 393;
Best Local Similarity 73.8%; Pred. No. 6.2e-20;
Matches 45; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 CGPGTKKVHVIFNYKGNVLINCKDIRCKDDFTHLYTLIVRPNTYEVKIDNSQVSGSL 60
DB 135 CGMATKKVHVIFNYKGNHLIKKIPCKDDLKTHLYTLIVPNPNKYEVLDNAKVESGSL 194
QY 61 E 61
DB 195 E 195
```

Db 143 CGYSTKKVHAI FNYNDTNHLIKDVPCEIDQLTHVYTFILRPDATYSILIDNQEKGQSGSL 202

Search completed: October 4, 2004, 13:06:34
Job time : 13.2765 secs

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RESULT 14
S25851
calreticulin precursor - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 06-Jan-1994 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999
C:Accession: S25851; T33996
R:Smith, M.J.
DNA Seq. 2, 235-240, 1992
A:Title: A. C. elegans gene encodes a protein homologous to mammalian calreticulin.
A:Reference number: S25851; MUID:92329978; PMID:1627827
A:Accession: S25851
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-395 <SMI>
A:Cross-references: EMBL:X59589; NID:96693; PIDN:CAA42159.1; PID:96694
R:Bauer, C.; Courtney, L.; Lapiant, Y.
submitted to the EMBL Data Library, February 1999
A:Description: The sequence of C. elegans cosmid Y38A10A.
A:Reference number: Z21453
A:Accession: T33996
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-395 <BAU>
A:Cross-references: EMBL:AF125963; PIDN:ADI4746.1; GSPDB:GNC00023; CESP:Y38A10A.5
A:Experimental source: Strain Bristol N2; Clone Y38A10A
C:Genetics:
A:Gene: CESP:Y38A10A.5
A:Map position: 5
A:Introns: 107/3; 315/3
C:Superfamily: calreticulin
F:1-15/Domain: signal sequence #status predicted <SIG>
F:792-395/Region: endoplasmic reticulum retention signal

Query Match 67.1%; Score 219.5; DB 2; Length 395;
Best Local Similarity 67.2%; Pred. No. 5.4e-18;
Matches 41; Conservative 7; Mismatches 12; Indels 1; Gaps 1;

QY 1 CGPGTKKHVIFNYKGNVLNIDIRCKDDEPHLYTLVRPDNTVEYVKIDNSQVESGSL 60
Db 133 CGP-TRRVHVLNLYAGENKIKKEITCKSDHLTHLYTLINSDNTVEYVKIDGESAQIGSL 191

QY 61 E 61
Db 192 E 192

RESULT 15
Ti4554
calreticulin - beet
C:Species: Beta vulgaris (beet)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Jun-2000
C:Accession: Ti4554
R:Viereck, R.
submitted to the EMBL Data Library, October 1997
A:Description: Nucleotide sequence from sugar beet calreticulin.
A:Reference number: Z18137
A:Accession: Ti4554
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-416 <VIE>
A:Cross-references: EMBL:AJ002057
A:Experimental source: strain diploide Inzuchtlinie KWS; leaf
C:Superfamily: calreticulin
C:Keywords: calcium binding

Query Match 59.0%; Score 193; DB 2; Length 416;
Best Local Similarity 56.7%; Pred. No. 7.3e-15;
Matches 34; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

QY 1 CGPGTKKHVIFNYKGNVLNIDIRCKDDEPHLYTLVRPDNTVEYVKIDNSQVESGSL 60
```

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OM protein - protein search, using sw model

Run on: October 4, 2004, 12:52:12 ; Search time 8.97059 Seconds
(without alignments)
354.077 Million cell updates/sec

Title: US-09-807-148-5
Perfect score: 327
Sequence: 1 CGEGTKKHVIFNYKGNVL.....PNTYEVKIDNSQVSGSL 61

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	327	100.0	416	1	CRTC_MOUSE
2	327	100.0	416	1	CRTC_MOUSE
3	327	100.0	417	1	CRTC_MOUSE
4	327	100.0	417	1	CRTC_MOUSE
5	327	100.0	418	1	CRTC_MOUSE
6	322	98.5	417	1	CRTC_MOUSE
7	322	98.5	421	1	CRTC_MOUSE
8	278	85.0	406	1	CRTC_MOUSE
9	251	76.8	388	1	CRTC_MOUSE
10	236	72.2	393	1	CRTC_MOUSE
11	219.5	67.1	395	1	CRTC_MOUSE
12	208	63.6	420	1	CRTC_MOUSE
13	193	59.0	416	1	CRTC_MOUSE
14	188	57.5	421	1	CRTC_MOUSE
15	186	56.9	415	1	CRTC_MOUSE
16	184	56.3	424	1	CRTC_MOUSE
17	184	56.3	384	1	CRTC_MOUSE
18	182	55.7	380	1	CRTC_MOUSE
19	181	55.4	425	1	CRTC_MOUSE
20	181	55.4	424	1	CRTC_MOUSE
21	180	55.0	424	1	CRTC_MOUSE
22	178	54.4	416	1	CRTC_MOUSE
23	175	53.5	424	1	CRTC_MOUSE
24	170	52.0	420	1	CRTC_MOUSE
25	169.5	51.8	401	1	CRTC_MOUSE
26	163	49.8	416	1	CRTC_MOUSE
27	117.5	35.9	592	1	CALX_MOUSE
28	116.5	35.6	591	1	CALX_MOUSE
29	116.5	35.6	591	1	CALX_MOUSE
30	115.5	35.3	593	1	CALX_MOUSE
31	107.5	32.9	610	1	CALX_MOUSE
32	106.5	32.6	611	1	CALX_MOUSE
33	101.5	31.0	619	1	CALX_MOUSE

34	99	30.3	560	1	CALX_MOUSE
35	90.5	27.7	545	1	CALX_MOUSE
36	85.5	26.1	530	1	CALX_MOUSE
37	80.5	24.6	540	1	CALX_MOUSE
38	80.5	24.6	551	1	CALX_MOUSE
39	75.5	23.1	532	1	CALX_MOUSE
40	73.5	22.5	540	1	CALX_MOUSE
41	61.5	18.8	582	1	CALX_MOUSE
42	61	18.7	474	1	CALX_MOUSE
43	60.5	18.5	586	1	CALX_MOUSE
44	59.5	18.2	220	1	CALX_MOUSE
45	59.5	18.2	220	1	CALX_MOUSE

ALIGNMENTS

RESULT 1

ID	CRTC_MOUSE	STANDARD	PRT	416 AA
AC	P14211			
DT	01-JAN-1990 (Rel. 13, Created)			
DT	01-JAN-1990 (Rel. 13, Last sequence update)			
DT	15-MAR-2004 (Rel. 43, Last annotation update)			
DE	Calreticulin precursor (CRP55) (Calregulin) (HACBP) (ERP50).			
GN	CALR.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 18-48 AND 129-161.			
RC	STRAIN=BALB/C; TISSUE=Liver;			
RX	MEDLINE=90059955; PubMed=2583110;			
RA	Smith M.J., Koch G.L.E.;			
RT	"Multiple zones in the sequence of calreticulin (CRP55, calregulin, HACBP), a major calcium binding ER/SR protein.";			
RL	EMBO J. 8:3581-3586(1989).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=93013037; PubMed=1398135;			
RA	Mazzarella R.A., Gold P., Cunningham M., Green M.;			
RT	"determination of the sequence of an expressible cDNA clone encoding Exp60/calregulin by the use of a novel nested set method.";			
RL	Gene 120:217-225(1992).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=FVB/N-3; TISSUE=Mammary gland;			
RX	MEDLINE=22398257; PubMed=12477932;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Moore H., Moore T., Max S.I., Wang J., Hsieh P.,			
RA	Hopkins R.F., Jordan H., Farmer A.A., Rubin G.M., Hong L.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Casavant T.L., Scheetz T.E.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,			
RA	Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalón D.K., Murry D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahey J., Helton B., Kettman M., Madan A., Rodriguez S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			
RA	Butterfield J.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,			
RA	Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
RN	[4]			
RP	SEQUENCE OF 18-38.			
RC	TISSUE=Fibroblast;			
RX	MEDLINE=95009907; PubMed=7523108;			

P36581	schizosacch
Q39817	glycine max
P29402	arabidopsis
Q39934	helianthus
O82709	pisum sativ
Q38798	arabidopsis
P25201	acinetobact
Q92777	homo sapien
P48680	mus musculu
P21619	mus musculu
Q63537	rattus norv
P40555	saccharomyc

RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
 RT "Separation and sequencing of familial and novel murine proteins
 using preparative two-dimensional gel electrophoresis.";
 RL Electrophoresis 15:735-745(1994).
 CC -!- FUNCTION: This protein binds calcium. There are both high and
 CC low affinity calcium-binding sites.
 CC -!- SUBUNIT: Monomer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
 CC -!- SIMILARITY: Belongs to the calreticulin family.
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 CC -----
 DR EMBL; X14926; CAA33053.1; -;
 DR EMBL; M92988; AAA37569.1; -;
 DR EMBL; BC003453; AAH03453.1; -;
 DR PIR; S06763; S06763;
 DR SWISS-PROT; P14211; MOUSE.
 DR MGD; MGI:88252; Calr.
 DR GO; GO:0005509; F:calcium ion binding; IDA.
 DR InterPro; IPR009033; Calret calnex P.
 DR InterPro; IPR001580; Calreticulin.
 DR InterPro; IPR008985; Cona like lec-gl.
 DR InterPro; IPR00886; ER target S.
 DR Pfam; PF00262; Calreticulin; 1.
 DR Pfam; PF00262; Calreticulin; 1.
 DR PRINTS; PR06266; CALRETICULIN.
 DR PRODom; PD001866; Calreticulin; 1.
 DR PROSITE; PS00014; ER TARGET; 1.
 DR PROSITE; PS00803; CALRETICULIN 1; 1.
 DR PROSITE; PS00804; CALRETICULIN 2; 1.
 DR PROSITE; PS00805; CALRETICULIN REPEAT; 3.
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
 FT SIGNAL 1 17
 FT CHAIN 18 416 CALRETICULIN.
 FT DOMAIN 18 197 N-DOMAIN.
 FT DOMAIN 198 308 P-DOMAIN.
 FT DOMAIN 309 416 C-DOMAIN.
 FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.
 FT REPEAT 191 202 1-1.
 FT REPEAT 202 221 1-2.
 FT REPEAT 221 238 1-3.
 FT REPEAT 238 255 1-4.
 FT REPEAT 259 297 3 X APPROXIMATE REPEATS.
 FT REPEAT 273 283 2-1.
 FT REPEAT 283 297 2-2.
 FT REPEAT 297 351 2-3.
 FT DOMAIN 351 407 ASP/GLY/LYS-RICH.
 FT DISULFID 127 163 BY SIMILARITY.
 FT SITE 413 PREVENT SECRETION FROM ER.
 FT SITE 416 24C03B00913408D8 CRC64;
 SQ SEQUENCE 416 AA; 47994 MW; 24C03B00913408D8 CRC64;
 Query Match 100.0%; Score 327; DB 1; Length 416;
 Best Local Similarity 100.0%; Pred. No. 1.2e-32;
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGPGTKKHVIFNYKGNVLINKIRCKDDEFTHTLVIRPNTVEYKIDNSQVSGSL 60
 Db 137 CGPGTKKHVIFNYKGNVLINKIRCKDDEFTHTLVIRPNTVEYKIDNSQVSGSL 196
 QY 61 E'61
 Db 197 E 197
 RESULT 2
 CRIC_RAT
 ID CRIC_RAT STANDARD; PRT; 416 AA.

AC P18418; F10452;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Calreticulin precursor (CRP55) (Calregulin) (HACBP) (BRP60) (CALBP)
 DE (Calcium-binding protein 3) (CABP3).
 GN CALR.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Brain cortex;
 RX MEDLINE=90370456; PubMed=2395661;
 RA Murthy K.K., Banville D., Srikant C.B., Carrier F., Bell A.,
 RA Holmes C., Patel Y.C.;
 RA "Structural homology between the rat calreticulin gene product and
 RT the Onchocerca volvulus antigen Ral-1.";
 RL Nucleic Acids Res. 18:4933-4933(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RX MEDLINE=93202172; PubMed=8453984;
 RA Nakamura M., Moriya M., Baba T., Michikawa Y., Yamanobe T., Arai K.,
 RA Okinaga S., Kobayashi T.;
 RA "An endoplasmic reticulum protein, calreticulin, is transported into
 RT the acrosome of rat sperm.";
 RL Exp. Cell Res. 205:101-110(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Liver;
 RX MEDLINE=95181573; PubMed=7876339;
 RA Soennichsen B., Fueflekrug J., van Nguyen P., Diekmann W.,
 RA Robinson D.G., Mieskes G.;
 RA Retention and retrieval: both mechanisms cooperate to maintain
 RT calreticulin in the endoplasmic reticulum.";
 RL J. Cell Sci. 107:2705-2717(1994).
 RN [4]
 RP SEQUENCE OF 270-358 FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RA Lone Y.C., Bailly A., Latruffe N.;
 RL Submitted (DEC-1988) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 18-29.
 RX MEDLINE=91054414; PubMed=2241926;
 RA Treves S., de Mattei M., Lanfredi M., Villa A., Green N.M.,
 RA Maciennan D.H., Meldolesi J., Pozzan T.;
 RT "Calreticulin is a candidate for a calsequestrin-like function in
 RL Ca2(+)-storage compartments (calciosomes) of liver and brain.";
 RL Biochem. J. 271:473-480(1990).
 RN [6]
 RP SEQUENCE OF 18-32.
 RC STRAIN=Sprague-Dawley; TISSUE=Testis;
 RX MEDLINE=92360010; PubMed=1497655;
 RA Nakamura M., Michikawa Y., Baba T., Okinaga S., Arai K.;
 RA "Calreticulin is present in the acrosome of spermatids of rat
 RT testis.";
 RL Biochem. Biophys. Res. Commun. 186:668-673(1992).
 RN [7]
 RP SEQUENCE OF 18-32.
 RC STRAIN=LEC; TISSUE=Liver;
 RX MEDLINE=94072621; PubMed=8251535;
 RA Yokoi T., Nagayama S., Kajiwara R., Kawaguchi Y., Horiuchi R.,
 RA Kamataki T.;
 RT "Identification of protein disulfide isomerase and calreticulin as
 RL autoantigenic antigens in LEC strain of rats.";
 RL Biochim. Biophys. Acta 1158:339-344(1993).
 CC -!- FUNCTION: This protein binds calcium. There are both high and low
 CC affinity calcium-binding sites.
 CC -!- SUBUNIT: Monomer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
 CC -!- SIMILARITY: Belongs to the calreticulin family.

CC -!- CAUTION: Was originally (Ref.2) thought to be D-beta-
CC hydroxybutyrate dehydrogenase.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; D78308; BAAL1345.1; -
CC EMBL; X53363; CAA37446.1; -
CC EMBL; X13702; CAA31987.1; ALT_SEQ.
CC EMBL; X73327; CAA5890.1; -
CC PIR; JH0819; JH0819.
CC PDB; 1HHN; 26-FEB-02.
CC PDB; 1K91; 12-OCT-02.
CC PDB; 1K9C; 12-OCT-02.
CC InterPro; IPR009033; Calret calnex_P.
CC InterPro; IPR001580; Calreticulin.
CC InterPro; IPR008985; ConA_like lec_gl.
CC InterPro; IPR00886; ER_target_S.
CC Pfam; PF00262; calreticulin; 1.
CC PRINTS; PS00014; ER_TARGET; 1.
CC PROSITE; PS00803; CALRETICULIN_1; 1.
CC PROSITE; PS00804; CALRETICULIN_2; 1.
CC PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
CC Endoplasmic reticulum; Calcium-binding; Repeat; Signal; 3D-structure.
CC SIGNAL 1 17
CC CHAIN 18 416 CALRETICULIN.
CC DOMAIN 18 197 N-DOMAIN.
CC DOMAIN 198 308 P-DOMAIN.
CC DOMAIN 309 416 C-DOMAIN.
CC REPEAT 191 255 4 X APPROXIMATE REPEATS.
CC REPEAT 210 221 1-1.
CC REPEAT 227 238 1-2.
CC REPEAT 244 255 1-3.
CC REPEAT 259 269 1-4.
CC REPEAT 273 283 2-1.
CC REPEAT 287 297 2-2.
CC REPEAT 351 407 ASP/GLU/LYS-RICH.
CC DISULFID 137 163 BY SIMILARITY.
CC SITE 413 416 PREVENT SECRETION FROM ER.
CC SEQUENCE 416 AA; 47995 MW; 286713CED31A2970 CRC64;
Query Match 100.0%; Score 327; DB 1; Length 416;
Best Local Similarity 100.0%; Pred. No. 1.2e-32;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGPGTKKHVIFNYKGNVLINKDIRCKDDEFTHTLYTLVIRPDNTYEVKIDNSQVESGSL 60
DB 137 CGPGTKKHVIFNYKGNVLINKDIRCKDDEFTHTLYTLVIRPDNTYEVKIDNSQVESGSL 196
QY 61 E 61
DB 197 E 197
RESULT 3
ID -CRTC CRIGR STANDARD; PRT; 417 AA.
AC Q8K3H7;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Calreticulin precursor (CRP55) (Calregulin) (HACBP) (ERp60).
GN CALR.

OS Cricetus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetus.
OX NCBI_TaxID=10029;
RN [1]
RP SEQUENCE FROM N.A.
RA Chung J.Y., Lee G.M.;
RL Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
CC -!- FUNCTION: This protein binds calcium. There are both high and low
CC affinity calcium-binding sites.
CC -!- SUBUNIT: Monomer.
CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -!- SIMILARITY: Belongs to the calreticulin family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AY100688; AAM48568.1; -
CC InterPro; IPR009033; Calret calnex_P.
CC InterPro; IPR001580; Calreticulin.
CC InterPro; IPR008985; ConA_like lec_gl.
CC InterPro; IPR00886; ER_target_S.
CC Pfam; PF00262; calreticulin; 1.
CC PIRSF; PIRSF002356; Calreticulin; 1.
CC PRINTS; PR00626; Calreticulin.
CC PRODOM; PD001866; Calreticulin; 1.
CC PROSITE; PS00803; CALRETICULIN_1; 1.
CC PROSITE; PS00804; CALRETICULIN_2; 1.
CC PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
CC Endoplasmic reticulum; Calcium-binding; Repeat; Glycoprotein; Signal.
CC SIGNAL 1 17 BY SIMILARITY.
CC CHAIN 18 417 CALRETICULIN.
CC DOMAIN 18 197 N-DOMAIN.
CC DOMAIN 198 308 P-DOMAIN.
CC DOMAIN 309 417 C-DOMAIN.
CC REPEAT 191 255 4 X APPROXIMATE REPEATS.
CC REPEAT 210 202 1-1.
CC REPEAT 227 238 1-2.
CC REPEAT 244 255 1-3.
CC REPEAT 259 297 1-4.
CC REPEAT 273 283 2-1.
CC REPEAT 287 297 2-2.
CC REPEAT 351 407 ASP/GLU/LYS-RICH.
CC DISULFID 137 163 BY SIMILARITY.
CC SITE 414 417 PREVENT SECRETION FROM ER (POTENTIAL).
CC SEQUENCE 417 AA; 48242 MW; D617DA37D14F2D45 CRC64;
Query Match 100.0%; Score 327; DB 1; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.2e-32;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGPGTKKHVIFNYKGNVLINKDIRCKDDEFTHTLYTLVIRPDNTYEVKIDNSQVESGSL 60
DB 137 CGPGTKKHVIFNYKGNVLINKDIRCKDDEFTHTLYTLVIRPDNTYEVKIDNSQVESGSL 196
QY 61 E 61
DB 197 E 197
RESULT 4
ID -CRTC HUMAN STANDARD; PRT; 417 AA.
AC P27797;

DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Calreticulin precursor (CRP55) (Calregulin) (HACBP) (ERp60).
GN CALR OR CRTG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=92013129; PubMed=1919005;
RA Rokeach L.A., Haselby J.A., Meilof J.F., Smeenk R.J., Unnasch T.R.,
RA Greene B.M., Hoch S.O.;
RT "Characterization of the autoantigen calreticulin.";
RL J. Immunol. 147:3031-3039 (1991).
RN [2]
RN SEQUENCE FROM N.A.
RX MEDLINE=90237213; PubMed=2332496;
RA McCaulliffe D.P., Lux F.A., Lieu T.S., Sanz I., Hanke J., Newkirk M.M.,
RA Bachinski L.L., Itoh Y., Siciliano M.J., Reichlin M., Sonthelmer R.D.,
RA Capra J.D.;
RT "Molecular cloning, expression, and chromosome 19 localization of a
RT human Ro/SS-A autoantigen.";
RL J. Clin. Invest. 85:1379-1391 (1990).
RN [3]
RN SEQUENCE FROM N.A.
RX MEDLINE=92129342; PubMed=1733953;
RA McCaulliffe D.P., Yang Y.S., Wilson J., Sonthelmer R.D., Capra J.D.;
RT "The 5' flanking region of the human calreticulin gene shares
RT homology with the human GRP78, GRP94, and protein disulfide isomerase
RT promoters.";
RL J. Biol. Chem. 267:2557-2562 (1992).
RN [4]
RN SEQUENCE FROM N.A.
RA Liu J., Peng X., Yuan J., Qiang B.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBSJ databases.
RN [5]
RN SEQUENCE FROM N.A.
RA Lamerdin J.B., McCreedy P.M., Stillwagen S., Ramirez M., Carrano A.;
RT "Characterization by genomic sequence analysis of a gene-rich 111 kb
RT region of 19p13.2 containing the human DNA repair gene, RAD23A.";
RL Submitted (MAR-1997) to the EMBL/GenBank/DBSJ databases.
RN [6]
RN SEQUENCE FROM N.A.
RC TISSUE=Eye, Pancreas, and Skin;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA Altschul S.F., Zeng B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [7]
RN SEQUENCE OF 18-36.
RX MEDLINE=9202034; PubMed=1911778;
RA Rojiani M.V., Finlay B.B., Gray V., Dedhar S.;
RT "In vitro interaction of a polypeptide homologous to human Ro/SS-A
RT antigen (calreticulin) with a highly conserved amino acid sequence in
the cytoplasmic domain of integrin alpha subunits.";
RL Biochemistry 30:9859-9866 (1991).
RN [8]
RN SEQUENCE OF 18-32.
RX MEDLINE=90380058; PubMed=2400400;
RA Krause K.H., Simerman H.K.B., Jones L.R., Campbell K.P.;
RT "Sequence similarity of calreticulin with a Ca2(+)-binding protein
RT that co-purifies with an ins(1,4,5)P3-sensitive Ca2+ store in HL-60
RT cells.";
RL Biochem. J. 270:545-548 (1990).
RN [9]
RN SEQUENCE OF 18-28.
RC TISSUE=Liver;
EX MEDLINE=93162045; PubMed=1286669;
RA Hochstrasser D.F., Frutiger S., Paquet N., Bairoch A., Ravier F.,
RA Pasquali C., Sanchez J.-C., Tissot J.-D., Bjellqvist B., Vargass R.,
RA Appel R.D., Hughes G.J.;
RT "Human liver protein map: a reference database established by
RT microsequencing and gel comparison.";
RL Electrophoresis 13:992-1001 (1992).
RN [10]
RN PARTIAL SEQUENCE OF 25-34; 56-62; 208-221 AND 273-278.
RC TISSUE=Keratinocytes;
RX MEDLINE=93162043; PubMed=1286667;
RA Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E.,
RA Vandekerckhove J.;
RT "Microsequences of 145 proteins recorded in the two-dimensional gel
RT protein database of normal human epidermal keratinocytes.";
RL Electrophoresis 13:960-969 (1992).
RN [11]
RN SEQUENCE OF 18-26.
RC TISSUE=Colon carcinoma;
RX MEDLINE=97295306; PubMed=9150948;
RA Ji H., Reid G.E., Moritz R.L., Eddes J.S., Burgess A.W., Simpson R.J.;
RT "A two-dimensional gel database of human colon carcinoma proteins.";
RL Electrophoresis 18:605-613 (1997).
CC -!- FUNCTION: This protein binds calcium. There are both high and low
CC affinity calcium-binding sites.
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -!- SIMILARITY: Belongs to the calreticulin family.
CC -!- CAUTION: Was originally (Ref.2) thought to be the 52 kDa Ro
CC autoantigen.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M84739; AAA51916.1; -
CC EMBL; M32294; AAA36582.1; -
CC EMBL; AY047586; AAL1126.1; -
CC EMBL; AD000092; AAB51176.1; -
CC EMBL; BC002500; AAB02500.1; -
CC EMBL; BC007911; AAB07911.1; -
CC EMBL; BC020493; AAB20493.1; -
CC PIR; A42330; A37047.
CC PDB; 2CLR; 31-MAR-95.
CC SWISS-2DPAGE; P27797; HUMAN
CC Aarhus/Ghent-2DPAGE; 9401; IEP.
CC HSC-2DPAGE; P27797; HUMAN.
CC PHCI-2DPAGE; P27797; -
CC PMMA-2DPAGE; P27797; -
CC Siena-2DPAGE; P27797; -
CC Genew; HGNC:1455; CALR.
CC MIM; 109091; -
CC GO; GO:006355; P-regulation of transcription, DNA-dependent; TAS.
CC InterPro; IPR009033; Calret_cainex_P.
CC InterPro; IPR001580; Calreticulin.
CC InterPro; IPR008985; ConA_like lec_gl.

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DR InterPro; IPR000886; ER_target_S.
DR Pfam; PF00262; Calreticulin; 1.
DR PIRSF; PIRSF002356; Calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00014; ER_TARGET; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal; 3D-structure.
FT SIGNAL 1 17
FT CHAIN 18 417 CALRETICULIN.
FT DOMAIN 18 197 N-DOMAIN.
FT DOMAIN 198 308 P-DOMAIN.
FT DOMAIN 309 417 C-DOMAIN.
FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.
FT REPEAT 191 202 1-1.
FT REPEAT 210 221 1-2.
FT REPEAT 227 238 1-3.
FT REPEAT 244 255 1-4.
FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.
FT REPEAT 259 269 2-1.
FT REPEAT 273 283 2-2.
FT REPEAT 287 297 2-3.
FT DOMAIN 351 408 ASP/GLU/LYS-RICH.
FT DISULFID 137 163 BY SIMILARITY.
FT SITE 414 417 PREVENT SECRETION FROM ER.
FT CONFLICT 35 35 MISSING (IN REF. 3)
SQ SEQUENCE 417 AA; 48141 MW; BC37C3C0F1054FB2 CRC64;

Query Match 100.0%; Score 327; DB 1; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.2e-32;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSPGKPKVHVFNFKGNVLNKKIRCKDDEFTHTLYLVPRDNTYEVKIDNSQVSGSL 60
Db 137 CSPGKPKVHVFNFKGNVLNKKIRCKDDEFTHTLYLVPRDNTYEVKIDNSQVSGSL 196

QY 61 E 61
Db 197 E 197

RESULT 5
CRTC_RABIT
ID CRTC_RABIT STANDARD; PRT; 418 AA.
AC P15253;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Calreticulin precursor (CRP55) (Calregulin) (HACBP) (ERP60).
GN CALR.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=slow-twitch skeletal muscle;
RX MEDLINE=90094320; PubMed=2600080;
RA Fliegel L., Burns K., MacLennan D.H., Reithmeier R.A.F., Michalak M.;
RT "Molecular cloning of the high affinity calcium-binding protein
RT (calreticulin) of skeletal muscle sarcoplasmic reticulum.";
RL J. Biol. Chem. 264:21522-21528 (1989).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=fast-twitch skeletal muscle;
RX MEDLINE=91282795; PubMed=2059224;
RA Fliegel L., Michalak M.;
RT "Fast-twitch and slow-twitch skeletal muscles express the same
RT isoform of calreticulin.";
RL Biochem. Biophys. Res. Commun. 177:979-984 (1991).
RN [3]

SEQUENCE OF 18-36.
RX MEDLINE=91054414; PubMed=2241926;
RA Treves S., de Mattei M., Lanfredi M., Villa A., Green N.M.,
RA MacLennan D.H., Melchiesi J., Pozzan T.;
RT "Calreticulin is a candidate for a calsequestrin-like function in
RT Ca2(+)-storage compartments (calciosomes) of liver and brain.";
RL Biochem. J. 271:473-480 (1990).
RN [4]
RP SEQUENCE OF 18-46.
RX MEDLINE=91201375; PubMed=2016321;
RA Milner R.E., Bakes S., Shemanko C., Carpenter M.R., Smillie L.,
RA Vance J.E., Opas M., Michalak M.;
RT "Calreticulin, and not calsequestrin, is the major calcium binding
RT protein of smooth muscle sarcoplasmic reticulum and liver endoplasmic
RT reticulum.";
RL J. Biol. Chem. 266:7155-7165 (1991).
RN [5]
RP PARTIAL SEQUENCE.
RX TISSUE=Lung;
RX MEDLINE=92002038; PubMed=1911780;
RA Quan S., Falick A.M., Williams D.E., Cashman J.R.;
RT "Evidence for complex formation between rabbit lung flavin-containing
RT monooxygenase and calreticulin.";
RL Biochemistry 30:9892-9900 (1991).
CC -!- FUNCTION: This protein binds calcium. There are both high and low
CC affinity calcium-binding sites.
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -!- SIMILARITY: Belongs to the calreticulin family.

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EMBL; J05138; AAA31188.1; -
PIR; A34154; A34154.
PIR; C33208; C33208.
PIR; S13046; S13046.
DR InterPro; IPR009033; Calret calnex_P.
DR InterPro; IPR001580; Calreticulin_P.
DR PIRSF; PIRSF008985; ConA_like_rec_gl.
DR InterPro; IPR000886; ER_target_S.
DR Pfam; PF00262; calreticulin; 1.
DR PIRSF; PIRSF002356; Calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00014; ER_TARGET; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
FT SIGNAL 1 17
FT CHAIN 18 418 CALRETICULIN.
FT DOMAIN 18 197 N-DOMAIN.
FT DOMAIN 198 308 P-DOMAIN.
FT DOMAIN 309 418 C-DOMAIN.
FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.
FT REPEAT 191 202 1-1.
FT REPEAT 210 221 1-2.
FT REPEAT 227 238 1-3.
FT REPEAT 244 255 1-4.
FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.
FT REPEAT 259 269 2-1.
FT REPEAT 273 283 2-2.
FT REPEAT 287 297 2-3.
FT DOMAIN 351 408 ASP/GLU/LYS-RICH.
FT DISULFID 137 163 BY SIMILARITY.
FT SITE 418 418 PREVENT SECRETION FROM ER.
FT VARIANT 35 35 E -> D.

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FT  CONFLICT  90      90      P -> T (IN REF. 5).
SQ  SEQUENCE  418 AA;  48275 MW;  B6082B689DC763A6 CRC64;

Query Match      100.0%; Score 327; DB 1; Length 418;
Best Local Similarity 100.0%; Pred. No. 1.2e-32;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1 CGPGTKKVVHVFNYKGNVLINKDIRKDEFFHLYTLIVRPNTYEVKIDNSQVSGSL 60
Db  137 CGPGTKKVVHVFNYKGNVLINKDIRKDEFFHLYTLIVRPNTYEVKIDNSQVSGSL 196

Qy  61 E 61
Db  197 E 197

RESULT 6
CRT1_BOVIN STANDARD; PRT; 417 AA.
AC  P52133; Q8S053;
DT  01-OCT-1996 (Rel. 34, Created)
DT  28-FEB-2003 (Rel. 41, Last sequence update)
DT  28-FEB-2003 (Rel. 41, Last annotation update)
DE  Calreticulin, brain isoform 1 precursor (CRP55) (Calregulin) (HACBP).
GN  CALR OR CRT.
OS  Bos taurus (Bovine).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC  Bovidae; Bovinae; Bos.
OX  NCBI_TaxID=9913;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  TISSUE=Brain;
RA  Hossain M.A., Takawa K., Minakata H., Nakajima T.;
RT  "Bovine brain calreticulin."
RL  Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN  [2]
RP  SEQUENCE OF 18-417.
RC  TISSUE=Brain;
RA  Matsuoka K., Seta K., Yamakawa Y., Okuyama T., Shinoda T., Isobe T.;
RT  "Covalent structure of bovine brain calreticulin."
RL  Biochem. J. 298:435-442(1994).
CC  -!- FUNCTION: This protein binds calcium. There are both high and low
CC  affinity calcium-binding sites.
CC  -!- SUBUNIT: Monomer.
CC  -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC  -!- SIMILARITY: Belongs to the calreticulin family.
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CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
CC  EMBL; AB067687; BAB86913.1;
CC  InterPro; IPR009033; Calret calnex P.
CC  InterPro; IPR001580; Calreticulin.
CC  InterPro; IPR008985; ConA_likelec-gl.
CC  Pfam; PF00262; calreticulin; 1.
CC  PRINTS; PRS002356; Calreticulin; 1.
CC  ProDom; PD018666; Calreticulin; 1.
CC  PROSITE; PS00014; ER TARGET; 1.
CC  PROSITE; PS00803; CALRETICULIN_1; 1.
CC  PROSITE; PS00804; CALRETICULIN_2; 1.
CC  PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
CC  Endoplasmic reticulum; Calcium-binding; Repeat; Glycoprotein; Signal.
FT  SIGNAL 1 17
FT  CHAIN 18 417 CALRETICULIN, BRAIN ISOFORM 1.

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FT  DOMAIN 18 197 N-DOMAIN.
FT  DOMAIN 198 308 P-DOMAIN.
FT  DOMAIN 309 417 C-DOMAIN.
FT  REPEAT 191 255 4 X APPROXIMATE REPEATS.
FT  REPEAT 210 221 1-1.
FT  REPEAT 227 238 1-2.
FT  REPEAT 244 255 1-3.
FT  REPEAT 259 297 1-4.
FT  REPEAT 297 269 3 X APPROXIMATE REPEATS.
FT  REPEAT 273 283 2-1.
FT  REPEAT 287 297 2-2.
FT  REPEAT 351 407 2-3.
FT  DOMAIN 137 163 ASP/GLU/LYS-RICH.
FT  DISULFID 137 163 N-LINKED (GLCNAC. .).
FT  CARBOHYD 179 179 PREVENT SECRETION FROM ER (POTENTIAL).
FT  SITE 414 417 PREVENT SECRETION FROM ER (POTENTIAL).
SQ  SEQUENCE 417 AA; 48038 MW; 7BF812C7B5417BE9 CRC64;

Query Match      98.5%; Score 322; DB 1; Length 417;
Best Local Similarity 98.4%; Pred. No. 4.9e-32;
Matches 60; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy  1 CGPGTKKVVHVFNYKGNVLINKDIRKDEFFHLYTLIVRPNTYEVKIDNSQVSGSL 60
Db  137 CGPGTKKVVHVFNYKGNVLINKDIRKDEFFHLYTLIVRPNTYEVKIDNSQVSGSL 196

Qy  61 E 61
Db  197 E 197

RESULT 7
CRT2_BOVIN STANDARD; PRT; 421 AA.
AC  P42918;
DT  01-NOV-1995 (Rel. 32, Created)
DT  01-NOV-1995 (Rel. 32, Last sequence update)
DT  15-JUL-1998 (Rel. 36, Last annotation update)
DE  Calreticulin, brain isoform 2 precursor (CRP55) (Calregulin) (HACBP).
OS  Bos taurus (Bovine).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC  Bovidae; Bovinae; Bos.
OX  NCBI_TaxID=9913;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  TISSUE=Brain;
RA  Liu N., Fine R.E., Johnson R.J.;
RT  "Comparison of cDNAs from bovine brain coding for two isoforms of
RT  calreticulin."
CC  -!- FUNCTION: This protein binds calcium. There are both high and low
CC  affinity calcium-binding sites.
CC  -!- SUBUNIT: Monomer (By similarity).
CC  -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC  -!- SIMILARITY: Belongs to the calreticulin family.
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
CC  EMBL; L13462; AAC37307.1;
CC  InterPro; IPR009033; Calret calnex P.
CC  InterPro; IPR001580; Calreticulin.
CC  InterPro; IPR008985; ConA_likelec-gl.
CC  InterPro; IPR008985; ConA_likelec-gl.
CC  Pfam; PF00262; calreticulin; 1.

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DR PIRSF; PIRSF002356; Calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR PRODOM; PD001866; Calreticulin; 1.
DR PROSITE; PS00014; ER_TARGET; 1.
DR PROSITE; PS00803; CALRETICULIN 1; 1.
DR PROSITE; PS00804; CALRETICULIN 2; 1.
DR PROSITE; PS00805; CALRETICULIN REPEAT; 3.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
FT SIGNAL 1 34
FT CHAIN 35 421
FT DOMAIN 35 201
FT DOMAIN 202 312
FT DOMAIN 313 421
FT DOMAIN 195 259
FT REPEAT 195 206
FT REPEAT 214 225
FT REPEAT 231 242
FT REPEAT 248 259
FT REPEAT 263 301
FT REPEAT 263 273
FT REPEAT 277 287
FT REPEAT 291 301
FT DOMAIN 366 411
FT DISULFID 141 167
FT CARBOHYD 183 183
FT SITE 418 421
SQ SEQUENCE 421 AA; 48812 MW; 0257E959F71528BC CRC64;

Query March 98.5%; Score 322; DB 1; Length 421;
Best Local Similarity 98.4%; Pred. No. 4.9e-32;
Matches 60; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGPOTKKVHVFYFKGNVLINLKIRCKDDEFTLYLTVRPNTYEVKIDNSQVSGSL 60
Db 141 CGPOTKKVHVFYFKGNVLINLKIRCKDDEFTLYLTVRPNTYEVKIDNSQVSGSL 200

Qy 61 E 61
Db 201 E 201

RESULT 8
ID CRTC DROME STANDARD; PRT; 406 AA.
AC P29413; Q9VHA3;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Calreticulin precursor (CRP55) (Calregulin) (HACBP).
GN CRC OR CG9429.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93208374; PubMed=1296819;
RA Smith M.J.;
RT "Nucleotide sequence of a Drosophila melanogaster gene encoding a
RL calreticulin homologue."
RL DNA Seq. 3:247-250(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celiniker S.E., Helt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Bfannkoch C., Baldwin D.,

RA Balaw R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.V., Benos P.V., Bertram B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Danke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fostler A., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kechum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J.R., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Massarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
RN [3]
RP SEQUENCE OF 91-124 AND 182-220.
RX MEDLINE=90307981; PubMed=2365822;
RA McCauliffe D.P., Zappi E., Lieu T.S., Michalak M., Sontheimer R.D.,
RA Capra J.D.;
RT "A human Ro/SS-A autoantigen is the homologue of calreticulin and is
RT highly homologous with onchocercal RAL-1 antigen and an aplysia
RT memory molecule."
RL J. Clin. Invest. 86:332-335(1990).
CC -!- FUNCTION: This protein binds calcium. There are both high and low
CC affinity calcium-binding sites.
CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -!- SIMILARITY: Belongs to the calreticulin family.
CC
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CC
CC EMBL; X64461; CAA45791.1; -.
CC EMBL; AE003683; AAF54416.1; -.
CC PIR; A56637; A56637.
CC FlyBase; FBgn0005585; Crc.
CC GO; GO:0007417; P:central nervous system development; IMP.
CC InterPro; IPR009033; Calret_calmex_P.
CC InterPro; IPR001580; Calreticulin.
CC InterPro; IPR008985; ConA_like_rec_gl.
CC InterPro; IPR000886; ER_target_S.
CC Pfam; PF00262; calreticulin; 1.
CC PIRSF; PIRSF002356; Calreticulin; 1.
CC PRINTS; PR00626; CALRETICULIN.
CC PRODOM; PD001866; Calreticulin; 1.
CC PROSITE; PS00014; ER_TARGET; 1.
CC PROSITE; PS00803; CALRETICULIN 1; 1.
CC PROSITE; PS00804; CALRETICULIN 2; 1.
CC PROSITE; PS00805; CALRETICULIN REPEAT; 3.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
FT SIGNAL 1 17
FT CHAIN 18 406
FT CHAIN CALRETICULIN.

FT CONFLICT 107 107 G -> A (IN REF. 3).
 FT CONFLICT 184 184 V -> L (IN REF. 3).
 SQ SEQUENCE 406 AA; 46808 MW; 65D72C69D0BEC427 CRC64;
 Query Match 85.0%; Score 278; DB 1; Length 406;
 Best Local Similarity 83.6%; Pred. No. 1.2e-26;
 Matches 51; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
 QY 1 CGPQTKVHVIFNYKGNVLINCKDKDEFHLYTLIVRPNTVEVKIDNSQVSGSL 60
 DB 137 CGPQTKVHVIFSYKGNHLISKDKDDVYTHFYTLIVRPNTVEVLIDNEKVSGL 196
 QY 61 E 61
 DB 197 E 197
 RESULT 9
 RALI_ONCVO STANDARD; PRT; 388 AA.
 AC P11012;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE RALI-1 protein precursor (41 kDa larval antigen).
 GN RALI.
 OS Onchocerca volvulus.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
 OC Onchocercidae; Onchocerca.
 OX NCBI_TaxID=6282;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94341871; PubMed=7520419;
 RA Rokeach L.A., Zimmerman P.A., Unnasch T.R.;
 RT "Epitopes of the Onchocerca volvulus RALI antigen, a member of the
 RT calreticulin family of proteins, recognized by sera from patients
 RT with onchocerciasis.";
 RL Infect. Immun. 62:3696-3704 (1994).
 RN [2]
 RP SEQUENCE OF 53-388 FROM N.A.
 RX MEDLINE=88273584; PubMed=2455736;
 RA Unnasch T.R., Gallin M.Y., Soboslay P.T., Ettmann K.D., Greene B.M.;
 RT "Isolation and characterization of expression cDNA clones encoding
 RT antigens of Onchocerca volvulus infective larvae.";
 RL J. Clin. Invest. 92:262-269 (1998).
 CC -!- SIMILARITY: Belongs to the calreticulin family.
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 CC -----
 CC EMBL; M20565; AAA59056.1; -;
 CC PIR; A32507; A32507.
 CC InterPro; IPR009033; Calret. calnex P.
 CC InterPro; IPR001580; Calreticulin.
 CC InterPro; IPR008985; ConAlike lec_gl.
 CC Pfam; PF00262; calreticulin; 1.
 CC PRINTS; PIRSF002356; Calreticulin; 1.
 CC PROSITE; PD001866; Calreticulin; 1.
 CC PROSITE; PD001866; Calreticulin; 1.
 CC PROSITE; PS00803; CALRETICULIN_1; 1.
 CC PROSITE; PS00804; CALRETICULIN_2; 1.
 CC PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
 CC Calcium-binding; Repeat; Antigen; Signal.
 CC SIGNAL 1 17
 CC POTENTIAL.
 FT CHAIN 18 388
 FT DOMAIN 189 253 4 X APPROXIMATE REPEATS.
 FT REPEAT 189 200 1-1.
 FT REPEAT 206 219 1-2.

FT REPEAT 225 236 1-3.
 FT REPEAT 242 253 1-4.
 FT DOMAIN 257 295 3 X APPROXIMATE REPEATS.
 FT REPEAT 257 267 2-1.
 FT REPEAT 271 281 2-2.
 FT REPEAT 285 295 2-3.
 FT DOMAIN 353 388 ARG/LYS-RICH (BASIC).
 FT DISULFID 135 161 BY SIMILARITY.
 SQ SEQUENCE 388 AA; 45298 MW; 9537F298A2D31CD6 CRC64;
 Query Match 76.8%; Score 251; DB 1; Length 388;
 Best Local Similarity 75.4%; Pred. No. 2.4e-23;
 Matches 46; Conservative 5; Mismatches 10; Indels 0; Gaps 0;
 QY 1 CGPQTKVHVIFNYKGNVLINCKDKDEFHLYTLIVRPNTVEVKIDNSQVSGSL 60
 DB 135 CGPQTKVHVIFHYKDRNMIKKDKDDVFTHLYTLIVNSDNTVEVDGKESGEL 194
 QY 61 E 61
 DB 195 E 195
 RESULT 10
 CRIC_SCHMA STANDARD; PRT; 393 AA.
 AC Q06814; Q26562;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Calreticulin precursor (SM4 protein).
 OS Schistosoma mansoni (Blood fluke).
 OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
 OC Schistosomatidae; Schistosomatidae; Schistosoma.
 OX NCBI_TaxID=6183;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=Puerto Rican;
 RX MEDLINE=93165070; PubMed=8433712;
 RA Khalife J., Trottein F., Schacht A.-M., Godin C., Pierce R.J.,
 RA Capron A.;
 RT "Cloning of the gene encoding a Schistosoma mansoni antigen
 RT homologous to human Ro/SS-A autoantigen.";
 RL Mol. Biochem. Parasitol. 57:193-202 (1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX STRAIN=Puerto Rican;
 RX MEDLINE=94187805; PubMed=8139623;
 RA Khalife J., Pierce R.J., Godin C., Capron A.;
 RT "Cloning and sequencing of the gene encoding Schistosoma mansoni
 RT calreticulin.";
 RL Mol. Biochem. Parasitol. 62:313-315 (1993).
 CC -!- FUNCTION: This protein binds calcium. There are both high and low
 CC affinity calcium-binding sites.
 CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
 CC -!- SIMILARITY: Belongs to the calreticulin family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC -----
 CC EMBL; M93097; AAA29854.1; -;
 CC EMBL; L24159; AAA19024.1; -;
 CC InterPro; IPR009033; Calret. calnex P.
 CC InterPro; IPR001580; Calreticulin.
 CC InterPro; IPR008985; ConAlike lec_gl.
 CC InterPro; IPR008986; ER_target_S.
 CC Pfam; PF00262; calreticulin; 1.
 CC PRINTS; PIRSF002356; Calreticulin; 1.
 CC FIRST; PIRSF002356; Calreticulin; 1.

Pfam; PF00262; calreticulin; 1.
DR PIRSF; PIRSF002356; Calreticulin; 1.
DR PRINTS; PRO0626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00014; ER TARGET; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 2.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal; Glycoprotein.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 421 CALRETICULIN.
FT CARBOHYD 56 56 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SITE 418 421 PREVENT SECRETION FROM ER (POTENTIAL).
FT SITE 421 421 PREVENT SECRETION FROM ER (POTENTIAL).
SQ SEQUENCE 421 AA; 48416 MW; 4FSF94CBAA6C6690 CRC64;

Query Match 57.5%; Score 188; DB 1; Length 421;
Best Local Similarity 55.0%; Pred. No. 1.5e-15;
Matches 33; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

Qy 1 CGPGTKKVHVIFNYKGNVLINCKDEFTLTVLRPDNTYEVKIDNSQVESGSL 60
Db 142 CGYSTKKVHALNNTNNLIKDVPCETDQLTHVTVFIIRPDATYSILIDNLEKQTGSL 201

RESULT 15
CRIC_RICCO STANDARD; PRT: 415 AA.
ID CRIC_RICCO
AC P93508;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Calreticulin precursor.
OS Ricinus communis (Castor bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Malpighiales; Euphorbiaceae; Acalyphoideae; Acalyphaceae;
OC Ricinus.
OX NCBI_TaxID=3988;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97435975; PubMed=9290642;
RA Coughlan S.J., Hastings C., Winfrey R. Jr.;
RT "Cloning and characterization of the calreticulin gene from Ricinus communis L.";
RL Plant Mol. Biol. 34:897-911(1997).
CC -!- FUNCTION: This protein binds calcium. There are both high and low
CC affinity calcium-binding sites.
CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -!- SIMILARITY: Belongs to the calreticulin family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U74631; AAB71420.1; -;
CC EMBL; U74630; AAB71419.1; -;
DR PIR; T10172; T10172.
DR InterPro; IPR009033; Calret_calmex_P.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR008985; ConA_like lec_g1.
DR InterPro; IPR00886; ER_target_S.
DR Pfam; PF00262; calreticulin; 1.
DR PIRSF; PIRSF002356; Calreticulin; 1.
DR PRINTS; PRO0626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00014; ER TARGET; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 2.

DR PROSITE; PS00805; CALRETICULIN_REPEAT; 2.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal; Glycoprotein.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 415 CALRETICULIN.
FT CARBOHYD 52 52 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 152 152 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SITE 412 415 PREVENT SECRETION FROM ER (POTENTIAL).
SQ SEQUENCE 415 AA; 47522 MW; DD5F452E76CC7F8C CRC64;

Query Match 56.9%; Score 186; DB 1; Length 415;
Best Local Similarity 53.3%; Pred. No. 2.5e-15;
Matches 32; Conservative 11; Mismatches 17; Indels 0; Gaps 0;

Qy 1 CGPGTKKVHVIFNYKGNVLINCKDEFTLTVLRPDNTYEVKIDNSQVESGSL 60
Db 138 CGYSTKKVHALNNTNNLIKDVPCETDQLTHVTVFIIRPDATYSILIDNLEKQTGSL 197

Search completed: October 4, 2004, 13:04:01
Job time : 9.97059 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 4, 2004, 12:52:42 ; Search time 36.9588 Seconds
(without alignments)
520.758 Million cell updates/sec

Title: US-09-807-148-5
Perfect score: 327
Sequence: 1 CGPCTKKVHVFNFKGNVL.....PNTVEVKIDNSQVSGSL 61

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues
Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL 25: *
1: sp_archaea: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
7: sp_nhc: *
8: sp_organelle: *
9: sp_phage: *
10: sp_plant: *
11: sp_rodent: *
12: sp_virus: *
13: sp Vertebrate: *
14: sp Unclassified: *
15: sp_virus: *
16: sp_bacteriap: *
17: sp_archaeap: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	303	92.7	318	13 Q9PTX7	Q9ptx7 lampetra re
2	290	88.7	405	5 Q26268	Q26268 aplysia cal
3	287	87.8	243	13 Q91711	Q91711 xenopus lae
4	287	87.8	411	13 Q91710	Q91710 xenopus lae
5	287	87.8	413	13 Q7ZW08	Q7zw08 xenopus lae
6	287	87.8	418	13 Q7ZYX3	Q7zyx3 xenopus lae
7	285	87.2	403	5 Q81S63	Q81s63 cotesia rub
8	284	86.9	407	5 Q86G72	Q86g72 dermacentor
9	280	85.6	406	5 Q8WR36	Q8wr36 anopheles g
10	279	85.3	421	5 Q9U6S0	Q9u6s0 strongyloce
11	278	85.0	406	5 Q9U916	Q9u916 drosophila
12	277	84.7	398	5 Q869E0	Q869e0 bombyx mori
13	277	84.7	398	5 Q7Z1E6	Q7z1e6 bombyx mori
14	276	84.4	397	5 Q8WPG8	Q8wpg8 gallieria me
15	276	84.4	410	5 Q16893	Q16893 amblyomma a
16	274	83.8	407	5 Q8T9U3	Q8t9u3 aedes aegypt

ALIGNMENTS

RESULT 1

Q9PTX7 PRELIMINARY; PRT; 318 AA.

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17      274      83.8      411      5      Q8MWP3
18      271      82.9      419      13      Q89884
19      268      82.0      417      13      Q9PUC1
20      265      81.0      423      13      Q7SZM3
21      263      80.4      417      13      Q802X3
22      258      78.9      387      5      Q97372
23      252      78.6      415      5      Q8MRU9
24      252      77.1      375      5      O18478
25      245.5      76.3      403      5      O76961
26      246      75.2      350      5      Q26514
27      246      75.2      396      5      Q45034
28      218      69.1      321      13      Q9USG0
29      218      66.7      395      5      Q96722
30      188      57.5      421      10      Q43712
31      188      57.5      442      10      Q7Y140
32      186      56.9      321      10      Q41799
33      185      56.6      412      10      Q40040
34      185      56.6      415      10      Q40041
35      183.5      56.1      427      10      Q9FYV2
36      183      56.0      425      10      Q8LJ85
37      182      55.7      137      11      Q9D373
38      182      55.7      272      11      Q8BL82
39      181      55.4      416      10      Q8H792
40      178      54.4      240      10      Q9ST29
41      178      54.4      389      10      Q40567
42      178      54.4      424      10      Q94AW7
43      178      54.4      424      10      Q8LC80
44      177      54.1      422      10      Q22502
45      176      53.8      380      10      Q7XAB5

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Q8MWP3 boophilus m
Q89884 rana rugosa
Q9PUC1 brachydanio
Q7SZM3 ictalurus p
Q802X3 brachydanio
Q97372 dirofilaria
Q8MRU9 meloidogyne
O18478 litomosoides
O76961 necator ame
Q26514 schistosoma
Q45034 schistosoma
Q9USG0 eptaretus
Q96722 taenia soli
Q43712 zea mays (m
Q7Y140 oryza sativ
Q41799 zea mays (m
Q40040 hordeum vul
Q40041 hordeum vul
Q9FYV2 pinus taeda
Q8LJ85 oryza sativ
Q9D373 mus musculu
Q8BL82 mus musculu
Q8H792 arabidopsis
Q9ST29 solanum mel
Q40567 nicotiana t
Q94AW7 arabidopsis
Q8LC80 arabidopsis
Q22502 brassica na
Q7XAB5 brassica ra

Query Match 92.7%; Score 303; DB 13; Length 318;

Best Local Similarity 91.8%; Pred. No. 1.2e-27;

Matches 56; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CGPCTKKVHVFNFKGNVLINKDKDEFTHLTYTLIVRPDNTVEVKIDNSQVSGSL 60

Matches 54; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
QY 1 CGPGTKKVVHVFYNYKGNVLINKDIRCKDDSFTHLYTLIVRPDNTYEVKIDNSQVSGSL 60
DB 132 CGPPTKKVHVIFQYKKKNLQINKDIRCKDDSFTHLYTLIVRPDNTYEVKIDNSKVESGSL 191
QY 61 E 61
DB 192 E 192
RESULT 5
Q7ZWU8 PRELIMINARY; PRT; 413 AA.
AC Q7ZWU8;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Similar to calreticulin.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.; to the EMBL/GenBank/DBJ databases.
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC046699; AAH46699.1; -.
DR GO; GO:0005514; F:calcium ion storage activity; IEA.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR009033; Calret calnex P.
DR InterPro; IPR008985; ConA like lec_gl.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 2.
DR PROSITE; PS00014; ER_TARGET; 1.
DR PROSITE; PS00014; ER_TARGET; 1.
SQ SEQUENCE 413 AA; 48521 MW; D8002F8F0523772B CRC64;
[1]
RP SEQUENCE FROM N.A.
Q7ZXV3 PRELIMINARY; PRT; 418 AA.
AC Q7ZXV3;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Similar to calreticulin.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
Query Match 87.8%; Score 287; DB 13; Length 413;
Best Local Similarity 88.5%; Pred. No. 1.3e-25;
Matches 54; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
QY 1 CGPGTKKVVHVFYNYKGNVLINKDIRCKDDSFTHLYTLIVRPDNTYEVKIDNSQVSGSL 60
DB 138 CGPPTKKVHVIFQYKKKNLQINKDIRCKDDSFTHLYTLIVRPDNTYEVKIDNSKVESGSL 197
QY 61 E 61
DB 198 E 198
RESULT 6
Q7ZXV3 PRELIMINARY; PRT; 418 AA.
AC Q7ZXV3;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Similar to calreticulin.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
Query Match 87.8%; Score 287; DB 13; Length 413;
Best Local Similarity 88.5%; Pred. No. 1.3e-25;
Matches 54; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
QY 1 CGPGTKKVVHVFYNYKGNVLINKDIRCKDDSFTHLYTLIVRPDNTYEVKIDNSQVSGSL 60
DB 138 CGPPTKKVHVIFQYKKKNLQINKDIRCKDDSFTHLYTLIVRPDNTYEVKIDNSKVESGSL 197
QY 61 E 61
DB 198 E 198

Klein S., Strausberg R.; to the EMBL/GenBank/DBJ databases.
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC044069; AAH44068.1; -.
DR GO; GO:0005514; F:calcium ion storage activity; IEA.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR009033; Calret calnex P.
DR InterPro; IPR008985; ConA like lec_gl.
DR InterPro; IPR000886; ER_target_S.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 2.
DR PROSITE; PS00014; ER_TARGET; 1.
DR PROSITE; PS00014; ER_TARGET; 1.
SQ SEQUENCE 418 AA; 49028 MW; 731C1C9AA0BF9A53 CRC64;
Query Match 87.8%; Score 287; DB 13; Length 418;
Best Local Similarity 88.5%; Pred. No. 1.3e-25;
Matches 54; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
QY 1 CGPGTKKVVHVFYNYKGNVLINKDIRCKDDSFTHLYTLIVRPDNTYEVKIDNSQVSGSL 60
DB 138 CGPPTKKVHVIFQYKKKNLQINKDIRCKDDSFTHLYTLIVRPDNTYEVKIDNSKVESGSL 197
QY 61 E 61
DB 198 E 198
RESULT 7
Q8IS63 PRELIMINARY; PRT; 403 AA.
ID Q8IS63;
AC Q8IS63;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Calreticulin.
DE Cotesia rubecula.
OC Cotesia rubecula.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Ichneumonidea;
OC Braconidae; Microgasterinae; Cotesia.
OX NCBI_TaxID=32392;
RN [1]
RP SEQUENCE FROM N.A.
RA Asgari S., Zhang G., Schmidt O.;
RT "Polydnavirus particle proteins with similarities to molecular
RT chaparons, heat shock protein 70 and calreticulin."
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AI50370; AAN73309.1; -.
DR GO; GO:0005514; F:calcium ion storage activity; IEA.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR009033; Calret calnex P.
DR InterPro; IPR008985; ConA like lec_gl.
DR InterPro; IPR000886; ER_target_S.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 2.
DR PROSITE; PS00014; ER_TARGET; 1.
DR PROSITE; PS00014; ER_TARGET; 1.
SQ SEQUENCE 403 AA; 46550 MW; 259D771A822DB126 CRC64;
Query Match 87.2%; Score 285; DB 5; Length 403;
Best Local Similarity 83.6%; Pred. No. 2.1e-25;
Matches 51; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
QY 1 CGPGTKKVVHVFYNYKGNVLINKDIRCKDDSFTHLYTLIVRPDNTYEVKIDNSQVSGSL 60
DB 136 CGPPTKKVHVIFQYKKKNLQINKDIRCKDDVTHLYTLIVRPDNTYEVKIDNEKVESGSL 195
QY 61 E 61

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Db      196 E 196

RESULT 8
Q86G72  PRELIMINARY;          PRT;    407 AA.
AC Q86G72;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Calreticulin.
OS Dermacentor variabilis.
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Parasitiformes; Ixodida; Ixodidae; Dermacentor.
OX NCBI_TaxID=34621;
RN [1]
RP SEQUENCE FROM N.A.
RA Simser J.A., Mulenga A., Macaluso K.R., Azad A.F.;
RT "Molecular characterization of Dermacentor variabilis calreticulin.";
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY241957; AAC92278.1; -.
DR GO; GO:0005514; F:calcium ion storage activity; IEA.
DR ProDom; PD00626; CALRETICULIN.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR009033; Calret calnex P.
DR InterPro; IPR008985; ConA like lec_gl.
DR InterPro; IPR00886; ER_target_S.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; CALRETICULIN.
DR ProDom; PD001866; CALRETICULIN.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
DR PROSITE; PS00014; ER_TARGET; 1.
DR PROSITE; PS00014; ER_TARGET; 1.
SQ SEQUENCE 407 AA; 47190 MW; FFE063AC49446E8 CRC64;

Query Match      86.9%; Score 284; DB 5; Length 407;
Best Local Similarity 85.2%; Pred. No. 2.8e-25;
Matches 52; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 CGPGTKKHVIFNYKGNVLINKDIRCKDDETHLYTLIVRPDNTYEVKIDNSQVESGSL 60
Db 136 CGPGTKKHVIFNYKGNVLINKDIRCKDDVFTHTLVVRADNTYEVLDNEKVESGSL 195

QY 61 E 61
Db 196 E 196

RESULT 9
Q8WR36  PRELIMINARY;          PRT;    406 AA.
AC Q8WR36;
DT 01-VAR-2002 (TREMBlrel. 20, Created)
DT 01-VAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-VAR-2002 (TREMBlrel. 25, Last annotation update)
DE Calreticulin.
OS Anopheles gambiae (African malaria mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
OX NCBI_TaxID=7165;
RN [1]
RP SEQUENCE FROM N.A.
RA Francischetti I.M., Valenzuela J.G., Ribeiro J.M.;
RT "Towards a catalog for genes and proteins from the salivary gland of
RT the malaria vector, Anopheles gambiae.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF457551; AAL68781.1; -.
DR GO; GO:0005514; F:calcium ion storage activity; IEA.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR009033; Calret calnex P.
DR InterPro; IPR008985; ConA like lec_gl.
DR InterPro; IPR00886; ER_target_S.

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DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
DR PROSITE; PS00014; ER_TARGET; 1.
SQ SEQUENCE 406 AA; 46285 MW; 85068FBCA9931F1 CRC64;

Query Match      85.6%; Score 280; DB 5; Length 406;
Best Local Similarity 85.2%; Pred. No. 8.3e-25;
Matches 52; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 CGPGTKKHVIFNYKGNVLINKDIRCKDDETHLYTLIVRPDNTYEVKIDNSQVESGSL 60
Db 134 CGPGTKKHVIFNYKGNVLINKDIRCKDDVFTHTLVVRADNTYEVLDNEKVESGSL 193

QY 61 E 61
Db 194 E 194

RESULT 10
Q9U6S0  PRELIMINARY;          PRT;    421 AA.
AC Q9U6S0;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Calreticulin precursor.
CN CALRET.
OS Strongylocentrotus purpuratus (Purple sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Echinoidea; Echinacea; Echinoida; Strongylocentrotidae;
OC Strongylocentrotus.
OX NCBI_TaxID=7668;
RN [1]
RP SEQUENCE FROM N.A.
RA Susan J.M., Just W.L., Lennarz W.J.;
RT "Cloning and Characterization of Alpha Integrin and Calreticulin in
RT Embryos of the Sea Urchin.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF177915; AAD55725.1; -.
DR GO; GO:0005514; F:calcium ion storage activity; IEA.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR009033; Calret calnex P.
DR InterPro; IPR008985; ConA like lec_gl.
DR InterPro; IPR00886; ER_target_S.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
DR PROSITE; PS00014; ER_TARGET; 1.
KW Signal.
FT SIGNAL.
FT CHAIN 1 19 POTENTIAL.
FT CHAIN 20 421 CALRETICULIN.
SQ SEQUENCE 421 AA; 48822 MW; 172C664F59F41F93 CRC64;

Query Match      85.3%; Score 279; DB 5; Length 421;
Best Local Similarity 80.3%; Pred. No. 1.1e-24;
Matches 49; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGPGTKKHVIFNYKGNVLINKDIRCKDDETHLYTLIVRPDNTYEVKIDNSQVESGSL 60
Db 136 CGPGTKKHVIFNYKGNVLINKDIRCKDDVFTHTLVVRADNTYEVLDNEKVESGSL 195

QY 61 E 61
Db 196 E 196

RESULT 11

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Q9U916
ID Q9U916 PRELIMINARY; PRT; 406 AA.
AC Q9U916, 2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Calreticulin.
GN OS Drosophila melanogaster (fruit fly).
OS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OREGON-R;
RA Dodo X., Sakoyana Y., Gamo S.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB000718; BAA85379.1; -
DR FlyBase; FBgn0005585; Crc.
DR GO; GO:0007417; P:central nervous system development; IMP.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR003033; Calreticulin.
DR InterPro; IPR008985; ConA_like_lcc_gi.
DR InterPro; IPR008986; ER_target_S.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
DR PROSITE; PS00014; ER_TARGET; 1.
SQ SEQUENCE 406 AA; 46809 MW; 68BA49A6B81CC427 CRC64;

Query Match 85.0%; Score 278; DB 5; Length 406;
Best Local Similarity 83.6%; Pred. No. 1.4e-24;
Matches 51; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CGPGTKKVHVFYNYKGNVLNKKDKDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSL 60
Db 137 CGPGTKKVHVFYNYKGNHLISKDKCKDDVYTHLYTLIVRPDNTYEVLDNKEVSGDL 196
Qy 61 E 61
Db 197 E 197

RESULT 12
ID Q869E0 PRELIMINARY; PRT; 398 AA.
AC Q869E0;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Calreticulin.
GN CRT.
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DAIZO; TISSUE=Fat body;
RA Takahashi T., Yamashita T.;
RL "Calreticulin expressed in fatbody of Bombyx mori.";
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB090887; BAC57964.1; -
DR GO; GO:0005514; F:calcium ion storage activity; IEA.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR009033; Calreticulin.
DR InterPro; IPR008985; ConA_like_lcc_gi.
RP SEQUENCE FROM N.A.

Qy 1 CGPGTKKVHVFYNYKGNVLNKKDKDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSL 60
Db 137 CGPGTKKVHVFYNYKGNHLISKDKCKDDVYTHLYTLIVRPDNTYEVLDNKEVSGDL 196
Qy 61 E 61
Db 197 E 197

RESULT 13
ID Q7Z1B6 PRELIMINARY; PRT; 398 AA.
AC Q7Z1B6;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Calreticulin.
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
RN [1]
RP SEQUENCE FROM N.A.
RA Kim S.R., Lee K.S., Kim I., Kang S.W., Nho S.K., Sohn H.D., Jin B.R.;
RL "Molecular cloning of a cDNA encoding putative calreticulin from the
RL silkworm, Bombyx mori.";
RL Int. J. Indust. Entomol. 6:93-97(2003).
DR EMBL; AY297158; AAP50845.1; -
SQ SEQUENCE 398 AA; 45801 MW; 0BC049839F5950EA CRC64;

Query Match 84.7%; Score 277; DB 5; Length 398;
Best Local Similarity 83.6%; Pred. No. 1.8e-24;
Matches 51; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CGPGTKKVHVFYNYKGNVLNKKDKDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSL 60
Db 137 CGPGTKKVHVFYNYKGNHLISKDKCKDDVYTHLYTLIVRPDNTYEVLDNKEVSGDL 196
Qy 61 E 61
Db 197 E 197

RESULT 14
ID Q8WPG8 PRELIMINARY; PRT; 397 AA.
AC Q8WPG8;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Calreticulin.
OS Galleria mellonella (Wax moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Pyraloidea;
OC Pyralidae; Galleriinae; Galleria.
OX NCBI_TaxID=7137;
RN [1]
RP SEQUENCE FROM N.A.
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GenCore version 5.1.6
Copyright (C) 1993 - 2004 Compugen Ltd.
OM protein - protein search, using sw model
Run on: October 4, 2004, 12:55:52 ; Search time 10.6647 Seconds
(without alignments)
441.961 Million cell updates/sec
Title: US-09-807-148-6
Perfect score: 258
Sequence: 1 NYGKGNVLNKDIRCKDDDF.....PDNTYEVKIDNSQVESGSLE 49
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : PIR_78.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	258	100.0	416	1 S06763	calreticulin precu
2	258	100.0	416	2 JH0819	calreticulin precu
3	258	100.0	417	1 A37047	calreticulin precu
4	258	100.0	418	1 A34154	calreticulin precu
5	253	98.1	400	2 S3376	calreticulin, brai
6	253	98.1	421	2 S36799	calreticulin precu
7	226	87.6	384	2 S29123	calreticulin (clon
8	226	87.6	411	2 S29123	calreticulin precu
9	221	85.7	405	1 JH0795	calreticulin precu
10	210	81.4	419	2 S71343	calreticulin precu
11	209	81.0	406	2 A56637	calreticulin homol
12	182	70.5	336	2 A32507	41K larval antigen
13	182	70.5	393	1 A48573	calreticulin autoa
14	179	69.4	395	2 S2581	calreticulin precu
15	148	57.4	421	2 S28170	calreticulin precu
16	144	55.8	412	2 T05703	calreticulin - bar
17	144	55.8	415	2 T05705	calreticulin - bar
18	144	55.8	416	2 T14554	calreticulin - bee
19	143	55.4	415	2 T10172	calreticulin - cas
20	138	53.5	425	2 C36605	calreticulin (ortl
21	135	52.3	389	2 T03691	calreticulin - com
22	135	52.3	416	2 T16968	calreticulin cal
23	135	52.3	444	2 H56224	hypothetical prote
24	134	51.9	422	2 T07841	probable calreticu
25	101	39.1	591	2 B54354	calnexin precursor
26	101	39.1	591	2 B54354	calnexin precursor
27	101	39.1	592	2 I32260	calnexin - human
28	101	39.1	592	2 A46673	calnexin precursor
29	100	38.8	593	1 A37273	calnexin precursor

ALIGNMENTS

RESULT 1
S06763
calreticulin precursor - mouse
N:Alternate names: 55K calcium-binding reticuloplasmin; calregulin
C:Species: Mus musculus (house mouse)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S06763; JCI1444; PC1233; A57498
R:Smith, M.J.; Koch, G.L.E.
EMBO J. 8, 3581-3586, 1989
A:Title: Multiple zones in the sequence of calreticulin (CRP55, calregulin, HACBP), a m
A:Reference number: S06763; MUID:90059955; PMID:2583110
A:Accession: S06763
A:Molecule type: DNA
A:Residues: 1-416 <SMI>
A:Cross-references: EMBL:X14926; NID:950567; PIDN:CAA33053.1; PID:950568
R:Mazzarella, R.A.; Gold, P.; Cunningham, M.; Green, M.
Gene 120, 217-225, 1992
A:Title: Determination of the sequence of an expressible cDNA clone encoding ERp60/calr
A:Reference number: JCI1444; MUID:93013037; PMID:1398135
A:Accession: JCI1444
A:Molecule type: mRNA
A:Residues: 1-416 <MAZ>
A:Cross-references: GB:M92988; NID:g193084; PIDN:AAA37569.1; PID:g193085
A:Accession: PC1233
A:Molecule type: protein
A:Residues: 18-41 <NA2>
R:White, T.K.; Zhu, Q.; Tanzer, M.L.
J. Biol. Chem. 270, 15926-15929, 1995
A:Title: Cell surface calreticulin is a putative mannoside lectin which triggers mouse
A:Reference number: A57498; MUID:95332280; PMID:7608143
A:Accession: A57498
A>Status: preliminary
A:Molecule type: Protein
A:Residues: 74-80;142-151;186-193 <WHI>
C:Superfamily: calreticulin
C:Keywords: calcium binding
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-416/Product: calregulin #status experimental <NAT>
F:413-416/Region: endoplasmic reticulum retention signal

Query Match 100.0%; Score 258; DB 1; Length 416;
Best Local Similarity 100.0%; Pred. No. 5.2e-24;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NYGKGNVLNKDIRCKDDDFTHLYTLIVRPDNTYEVKIDNSQVESGSLE 49
DB 149 NYGKGNVLNKDIRCKDDDFTHLYTLIVRPDNTYEVKIDNSQVESGSLE 197
RESULT 2
JH0819
calreticulin precursor - rat

N:Alternate names: calcium-binding protein 3
C:Species: Rattus norvegicus (Norway rat)
C>Date: 30-Sep-1993 #sequence revision 20-Aug-1994 #text change 20-Jun-2000
C:Accession: JH0819; A49176; S11205; PC1109; S45036; S04867; S39372; S13045
R:Nakamura, M.; Moriya, M.; Baba, T.; Michikawa, Y.; Yamanobe, T.; Arai, K.; Okinaga, S.
Exp. Cell Res. 205, 101-110, 1993
A>Title: An endoplasmic reticulum protein, calreticulin, is transported into the acrosome
A:Reference number: A49176; MUID:93202172; PMID:8453984
A:Accession: JH0819
A:Molecule type: mRNA
A:Residues: 1-416 <NAK>
A:Cross-references: GB:D78308; NID:G1089798; PIDN:BAAL11345.1; PID:G1845572
A:Accession: A49176
A>Status: preliminary
A:Molecule type: mRNA; protein
A:Residues: 1-416 <NA2>
A:Cross-references: GB:D78308; NID:G1089798; PIDN:BAAL11345.1; PID:G1845572
A:Experimental source: Sprague-Dawley, spermatogenic cells
A:Note: sequence extracted from NCBI backbone (NCBIN:127639, NCBI:P127643)
R:Murthy, K.K.; Banville, D.; Srikanth, C.B.; Carrier, F.; Holmes, C.; Bell, A.; Patel, Y.
Nucleic Acids Res. 18, 4933, 1990
A>Title: Structural homology between the rat calreticulin gene product and the Onchoerca
A:Reference number: S11205; MUID:90370496; PMID:2395661
A:Accession: S11205
A:Molecule type: mRNA
A:Residues: 1-416 <MUR>
A:Cross-references: EMBL:X53363; NID:G55854; PIDN:CAA37446.1; PID:G55855
R:Nakamura, M.; Michikawa, Y.; Baba, T.; Okinaga, S.; Arai, K.
Biochem. Biophys. Res. Commun. 186, 668-673, 1992
A>Title: Calreticulin is present in the acrosome of spermatozoa of rat testis.
A:Reference number: PC1109; MUID:92360010; PMID:1497655
A:Accession: PC1109
A:Molecule type: protein
A:Residues: 18-32 <NAK2>
R:Soennichsen, B.; Fuellekrug, J.; van Nguyen, P.; Diekmann, W.; Robinson, D.G.; Mieskes
submitted to the EMBL data library, May 1994
A:Description: Retention and retrieval: both mechanisms cooperate to maintain calreticulin
A:Reference number: S45036
A:Accession: S45036
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-416 <SOE>
A:Cross-references: EMBL:X79327; NID:G4988840; PIDN:CAA55890.1; PID:G4988941
R:Jone, Y.C.; Bailly, A.; Latruffe, N.
submitted to the EMBL Data Library, December 1988
A:Reference number: S04867
A:Accession: S04867
A:Molecule type: mRNA
A:Residues: 18-270-358, 'AAG' <LON>
A:Cross-references: EMBL:X13702; NID:G56055; PIDN:CAA31987.1; PID:G930260
A:Note: the authors designated the protein as D-beta-hydroxybutyrate dehydrogenase
R:Yokoi, T.; Nagayama, S.; Kajiwara, R.; Kawaguchi, Y.; Horiuchi, R.; Kamataki, T.
Biochim. Biophys. Acta 1158, 339-344, 1993
A>Title: Identification of protein disulfide isomerase and calreticulin as autoimmune an
A:Reference number: S39371; MUID:94072621; PMID:8251535
A:Accession: S39372
A:Molecule type: protein
A:Residues: 18-23, 'X', 25-32 <YOK>
R:Van, P.N.; Peter, F.; Soeling, H.D.
J. Biol. Chem. 264, 17494-17501, 1989
A>Title: Four intracisternal calcium-binding glycoproteins from rat liver microsomes with
active calcium sequestering rat liver vesicles
A:Reference number: A34473; MUID:90008920; PMID:2793869
A:Accession: A34473
A>Status: preliminary
A:Molecule type: protein
A:Residues: 18-36 <VAN>
R:Trevies, S.; de Mattei, M.; Lanfredi, M.; Villa, A.; Green, N.M.; MacLennan, D.H.; Meld
Biochem. J. 271, 473-480, 1990
A>Title: Calreticulin is a candidate for a calsequestrin-like function in Ca(2+)-storage
A:Reference number: S13045; MUID:91054414; PMID:2241926
A:Accession: S13045

A:Molecule type: protein
A:Residues: 18-29 <TRB>
C:Superfamily: calreticulin
C:Keywords: calcium binding; glycoprotein
F:1-17/Domain: signal sequence #status Predicted <SIG>
F:18-416/Product: calreticulin #status experimental <MAT>
F:204-212/Region: nuclear location signal
F:413-416/Region: endoplasmic reticulum retention signal
F:344/Binding site: carbohydrate (Asn) (covalent) #status Predicted

Query Match 100.0%; Score 258; DB 2; Length 415;
Best Local Similarity 100.0%; Pred. NO. 5.2e-24;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYKGNVLINKIRCKDETHLYTLIVRPDNTYEVKIDNSQVESGSL 49
149 NYKGNVLINKIRCKDETHLYTLIVRPDNTYEVKIDNSQVESGSL 197

RESULT 3

A37047
calreticulin precursor - human
N:Alternate names: 52K ribonucleoprotein autoantigen Ro/SS-A; 60K integrin-binding prote
C:Species: Homo sapiens (man)
C>Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 18-Feb-2000
C:Accession: A42330; A37047; A46452; A28812; PH1525; A40346; S1475; T45075
R:McCauffe, D.P.; Yang, Y.S.; Wilson, J.; Sontheimer, R.D.; Capra, J.D.
J. Biol. Chem. 267, 2557-2562, 1992
A>Title: The 5'-flanking region of the human calreticulin gene shares homology with the
A:Reference number: A42330; MUID:92129342; PMID:1733953
A:Accession: A42330
A:Molecule type: DNA
A:Residues: 1-417 <MC2>
A:Note: sequence extracted from NCBI backbone (NCBIN:78537, NCBI:P78536)
R:McCauffe, D.P.; Lux, F.A.; Lieu, T.S.; Sanz, I.; Hanke, J.; Newkirk, M.M.; Bachinski
J. Clin. Invest. 85, 1379-1391, 1990
A>Title: Molecular cloning, expression, and chromosome 19 localization of a human Ro/SS-
A:Reference number: A37047; MUID:90237213; PMID:2332496
A:Accession: A37047
A:Molecule type: mRNA
A:Residues: 1-417 <MCC>
A:Cross-references: GB:M32294; NID:G337486; PIDN:AAA36582.1; PID:G337487
A:Note: the authors translated the codon GTA for residue 349 as Tyr
R:Rokeach, L.A.; Haselby, J.A.; Meilof, J.F.; Smeenk, R.J.; Unnasch, T.R.; Greene, B.M.;
J. Immunol. 147, 3031-3039, 1991
A>Title: Characterization of the autoantigen calreticulin.
A:Reference number: A46452; MUID:92013129; PMID:1919005
A:Accession: A46452
A:Molecule type: mRNA
A:Residues: 1-417 <ROK>
A:Cross-references: GB:M84739; NID:G179881; PIDN:AAA51916.1; PID:G179882
A:Note: sequence extracted from NCBI backbone (NCBIN:60749, NCBI:P60750)
R:Lieu, T.S.; Newkirk, M.M.; Capra, J.D.; Sontheimer, R.D.
J. Clin. Invest. 82, 96-101, 1988
A>Title: Molecular characterization of the autoantigen calreticulin.
A:Reference number: A28812; MUID:88273610; PMID:3260607
A:Accession: A28812
A:Molecule type: protein
A:Residues: 18-41 <LIE>
A:Note: 18-Ala was also found
R:Dupuis, M.; Schaefer, E.; Krause, K.H.; Tschopp, J.
J. Exp. Med. 177, 1-7, 1993
A>Title: The calcium-binding protein calreticulin is a major constituent of lytic granul
A:Reference number: PH1525; MUID:93115648; PMID:8418194
A:Accession: PH1525
A:Molecule type: protein
A:Residues: 18-27 <DUP>
A:Experimental source: LAK cell
R:RoJani, M.V.; Finlay, B.B.; Gray, V.; Dedhar, S.
Biochemistry 30, 9859-9866, 1991
A>Title: In vitro interaction of a polypeptide homologous to human Ro/SS-A antigen (cal
A:Reference number: A40346; MUID:92002034; PMID:1911778
A:Accession: A40346

A;Molecule type: protein
A;Residues: 18-34; R' <ROJ>
R;Krause, K.H.; Simmerman, H.K.B.; Jones, L.R.; Campbell, K.P.
Biochem. J. 270, 545-548, 1990
A;Title: Sequence similarity of calreticulin with a Ca(2+)-binding protein that co-purifies with the endoplasmic reticulum chaperone BiP
A;Reference number: S11475; MUID:90380058; PMID:2400400
A;Accession: S11475
A;Molecule type: protein
A;Residues: 18-32 <KRA>
R;Lamerdin, J.; McCready, P.; Stilwagen, S.; Ramirez, M.; Carrano, A.
Submitted to the EMBL Data Library, November 1996
A;Description: Characterization by genomic sequence analysis of a gene-rich 111 kb region on human chromosome 12p13.3
A;Reference number: 222906
A;Accession: T45075
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-417 <LAM>
A;Cross-references: EMBL:AD000092; PIDN:AAB51176.1
A;Experimental source: cell line SHL2-B; fibroblast
A;Comment: Autoantibodies specific for this protein are found in Sjogren's syndrome and in other autoimmune diseases
A;Gene: GDB:CALR
A;Cross-references: GDB:125179; OMIM:109091
A;Map position: 19p13.3-19p13.2
A;Introns: 31/1; 65/1; 133/1; 164/3; 234/3; 272/3; 320/3; 351/3
A;Note: CRTC
C;Superfamily: calreticulin
C;Keywords: calcium binding; integrin binding
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-417/Product: calreticulin #status predicted <MAT>
F;414-417/Region: endoplasmic reticulum retention signal
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Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 149 NYKGNVLINKDIRCKDEFTHTLVIRPDNTYEVKIDNSQVSGSLE 197
RESULT 4
A34154
calreticulin precursor, skeletal muscle - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
A;Accession: A34154; S13047
R;Fliegel, L.; Burns, K.; MacLennan, D.H.; Reithmeier, R.A.F.; Michalak, M.
J. Biol. Chem. 264, 21522-21528, 1989
A;Title: Molecular cloning of the high affinity calcium-binding protein (calreticulin) cDNA from rabbit skeletal muscle
A;Reference number: A34154; MUID:90094320; PMID:2600080
A;Accession: A34154
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-418 <FLI>
A;Cross-references: GB:J05139; NID:G164859; PIDN:AAA31188.1; PID:G164859
R;Treves, S.; de Mattei, M.; Lanfredi, M.; Villa, A.; Green, N.M.; MacLennan, D.H.; Meldolesi, J.
Biochem. J. 271, 473-480, 1990
A;Title: Calreticulin is a candidate for a caldesmon-like function in Ca(2+)-storage vesicles
A;Reference number: S13045; MUID:91054414; PMID:2241926
A;Accession: S13047
A;Molecule type: protein
A;Residues: 19-32 <TRE>
C;Superfamily: calreticulin
C;Keywords: skeletal muscle
F;1-17/Domain: signal sequence #status predicted <SIG>
F;415-418/Region: endoplasmic reticulum retention signal
Query Match 100.0%; Score 258; DB 1; Length 418;
Best Local Similarity 100.0%; Pred. No. 5.3e-24;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NYKGNVLINKDIRCKDEFTHTLVIRPDNTYEVKIDNSQVSGSLE 49

DB 149 NYKGNVLINKDIRCKDEFTHTLVIRPDNTYEVKIDNSQVSGSLE 197
RESULT 5
S43376
calreticulin, brain isoform 1 - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 20-Oct-1994 #sequence_revision 23-Mar-1995 #text_change 07-May-1999
A;Accession: S43376; S36801
R;Matsuoka, K.; Seta, K.; Yamakawa, Y.; Okuyama, T.; Shinoda, T.; Isobe, T.
Biochem. J. 298, 435-442, 1994
A;Title: Covalent structure of bovine brain calreticulin.
A;Reference number: S43376; MUID:94183174; PMID:8135753
A;Accession: S43376
A;Molecule type: protein
A;Residues: 1-400 <MAT>
A;Experimental source: brain
R;Liu, N.; Fine, R.E.; Johnson, R.J.
Biochim. Biophys. Acta 1202, 70-76, 1993
A;Title: Comparison of cDNAs from bovine brain coding for two isoforms of calreticulin
A;Reference number: S36799; MUID:93385184; PMID:8373827
A;Accession: S36801
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 45-63; E', 65-83 <LIU>
A;Experimental source: brain, clone 8.1
C;Superfamily: calreticulin
C;Keywords: calcium binding; glycoprotein
F;137-400/Region: endoplasmic reticulum retention signal
F;120-146/Disulfide bonds: #status experimental
F;162/Binding site: carbohydrate (Asn) (covalent) #status experimental
Query Match 98.1%; Score 253; DB 2; Length 400;
Best Local Similarity 98.0%; Pred. No. 2.1e-23;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 NYKGNVLINKDIRCKDEFTHTLVIRPDNTYEVKIDNSQVSGSLE 49
DB 132 NYKGNVLINKDIRCKDEFTHTLVIRPDNTYEVKIDNSQVSGSLE 180
RESULT 6
S36799
calreticulin precursor, brain isoform 2 - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 10-Dec-1993 #sequence_revision 23-Mar-1995 #text_change 13-Aug-1999
A;Accession: S36799; S36800
R;Liu, N.; Fine, R.E.; Johnson, R.J.
Biochim. Biophys. Acta 1202, 70-76, 1993
A;Title: Comparison of cDNAs from bovine brain coding for two isoforms of calreticulin
A;Reference number: S36799; MUID:93385184; PMID:8373827
A;Accession: S36799
A;Molecule type: mRNA
A;Residues: 1-421 <LIU>
A;Cross-references: GB:U13462; NID:G348693; PIDN:AAC37307.1; PID:G348694
A;Experimental source: brain, clone 9.4
A;Accession: S36800
A;Molecule type: protein
A;Residues: 35-45 <LI2>
C;Superfamily: calreticulin
C;Keywords: calcium binding; glycoprotein
F;1-34/Domain: signal sequence #status predicted <SIG>
F;35-421/Product: calreticulin, brain isoform 2 #status predicted <MAT>
F;418-421/Region: endoplasmic reticulum retention signal
F;441-167/Disulfide bonds: #status predicted
F;193/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 98.1%; Score 253; DB 2; Length 421;
Best Local Similarity 98.0%; Pred. No. 2.2e-23;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 NYKGNVLINKDIRCKDEFTHTLVIRPDNTYEVKIDNSQVSGSLE 49

```

Db      153 NYKGNVLNKKIRCKDDFTHTLTVLRPNNTYEVKIDNSQVSGSLE 201
|||||
RESULT 7
S29130
calreticulin (clone 8) - African clawed frog (fragment)
C:Species: Xenopus laevis (African clawed frog)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
C:Accession: S29130; T01068
R:Treves, S.; Zorzato, F.; Pozzan, T.
Biochem. J. 287, 579-581, 1992
A>Title: Identification of calreticulin isoforms in the central nervous system.
A:Reference number: S29129; MUID:93074997; PMID:1445218
A:Accession: S29130
A:Molecule type: mRNA
A:Residues: 1-384 <TR>
A:CROSS-references: EMBL:X67598
A:Accession: T01068
A:Molecule type: mRNA
A:Status: translated from GB/EMBL/DDBJ
A:Residues: 1-339, 'XTGR' <TR>
A:CROSS-references: EMBL:X67598; NID:G64610; PIDN:CAA47867.1; PID:G64611
A:Experimental source: CNS
A:Superfamily: calreticulin
C:Keywords: glycoprotein
F:316/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match      87.6%; Score 226; DB 2; Length 384;
Best Local Similarity 89.6%; Pred. No. 4.2e-20;
Matches 43; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy      2 YKGNVLNKKIRCKDDFTHTLTVLRPNNTYEVKIDNSQVSGSLE 49
|||
Db      122 YKKNLQINKIRCKDDFTHTLTVLRPNNTYEVKIDNSQVSGSLE 169
|||||

RESULT 8
S29129
calreticulin precursor (clone 3) - African clawed frog (fragment)
C:Species: Xenopus laevis (African clawed frog)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
C:Accession: S29129
R:Treves, S.; Zorzato, F.; Pozzan, T.
Biochem. J. 287, 579-581, 1992
A>Title: Identification of calreticulin isoforms in the central nervous system.
A:Reference number: S29129; MUID:93074997; PMID:1445218
A:Accession: S29129
A:Molecule type: mRNA
A:Residues: 1-411 <TR>
A:CROSS-references: EMBL:X67597; NID:G64608; PIDN:CAA47866.1; PID:G64609
C:Superfamily: calreticulin
C:Keywords: glycoprotein
F:1-12/Domain: signal sequence (fragment) #status predicted <SIG>
F:13-411/Product: calreticulin #status predicted <MAT>
F:408-411/Region: endoplasmic reticulum retention signal
F:339/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match      87.6%; Score 226; DB 2; Length 411;
Best Local Similarity 89.6%; Pred. No. 4.5e-20;
Matches 43; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy      2 YKGNVLNKKIRCKDDFTHTLTVLRPNNTYEVKIDNSQVSGSLE 49
|||
Db      145 YKKNLQINKIRCKDDFTHTLTVLRPNNTYEVKIDNSQVSGSLE 192
|||||

RESULT 9
JH0795
calreticulin precursor - California sea hare
N:Alternate names: protein 407
C:Species: Aplysia californica (California sea hare)

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C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: JH0795; B31409; F60977
R:Kennedy, T.E.; Kuhl, D.; Barzilai, A.; Sweatt, J.D.; Kandel, E.R.
Neuron 9, 1013-1024, 1992
A>Title: Long-term sensitization training in aplysia leads to an increase in calreticulin
A:Reference number: JH0795; MUID:93098937; PMID:1463604
A:Accession: JH0795
A:Molecule type: mRNA
A:Residues: 1-405 <KEN>
A:CROSS-references: GB:S51239; NID:G262053; PIDN:AAB24569.1; PID:G262054
A:Experimental source: abdominal ganglion and antral nervous system
R:Kennedy, T.E.; Gawinowicz, M.A.; Barzilai, A.; Kandel, E.R.; Sweatt, J.D.
Proc. Natl. Acad. Sci. U.S.A. 85, 7008-7012, 1988
A>Title: Sequencing of proteins from two-dimensional gels by using in situ digestion and
A:Reference number: A94207; MUID:88320566; PMID:3413132
A:Accession: B31409
A:Molecule type: protein
A:Residues: 'X', 17-28, 'X', 30-31 <KE2>
R:Sweatt, J.D.; Kennedy, T.E.; Wager-Smith, K.; Gawinowicz, M.A.; Barzilai, A.; Karl, K.
Electrophoresis 10, 152-157, 1989
A>Title: Development of a database of amino acid sequences for proteins identified and
A:Reference number: A60977; MUID:89276284; PMID:2731514
A:Accession: F60977
A:Molecule type: protein
A:Residues: 'X', 17-28, 'X', 30-31 <SWE>
C:Superfamily: calreticulin
C:Keywords: calcium binding; endoplasmic reticulum
F:1-15/Domain: signal sequence #status predicted <SIG>
F:16-405/Product: calreticulin #status experimental <MAT>
F:402-405/Region: endoplasmic reticulum retention signal
Query Match      85.7%; Score 221; DB 1; Length 405;
Best Local Similarity 81.6%; Pred. No. 1.8e-19;
Matches 40; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy      1 NYKGNVLNKKIRCKDDFTHTLTVLRPNNTYEVKIDNSQVSGSLE 49
|||||
Db      145 NYKGNLQINKIRCKDDFTHTLTVLRPNNTYEVKIDNSQVSGSLE 193
|||||

RESULT 10
S71343
calreticulin precursor - Korean frog
C:Species: Rana rugosa (Korean frog)
C>Date: 29-Jan-1998 #sequence_revision 13-Feb-1998 #text_change 20-Jun-2000
C:Accession: S71343
R:Yamamoto, S.; Nakamura, M.
FEBS Lett. 387, 27-32, 1996
A>Title: Calnexin: its molecular cloning and expression in the liver of the frog, Rana
A:Reference number: S71342; MUID:96234004; PMID:8654561
A:Accession: S71343
A:Molecule type: mRNA
A:Status: nucleic acid sequence not shown
A:Residues: 1-419 <YAM>
A:CROSS-references: EMBL:D78589; NID:G1514956; PIDN:BAAL1425.1; PID:G1514957
C:Superfamily: calreticulin
C:Keywords: calcium binding; endoplasmic reticulum
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-419/Product: calreticulin #status predicted <MAT>
F:205-213/Region: nuclear location signal
F:415-418/Region: endoplasmic reticulum retention signal
Query Match      81.4%; Score 210; DB 2; Length 419;
Best Local Similarity 81.6%; Pred. No. 4.3e-18;
Matches 40; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy      1 NYKGNVLNKKIRCKDDFTHTLTVLRPNNTYEVKIDNSQVSGSLE 49
|||||
Db      150 NYKGNLQINKIRCKDDFTHTLTVLRPNNTYEVKIDNSQVSGSLE 198
|||||

RESULT 11

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[illegible]

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Mol. Biochem. Parasitol. 57, 193-202, 1993
A>Title: Cloning of the gene encoding a Schistosoma mansoni antigen homologous to human calreticulin precursor - Caenorhabditis elegans
A>Reference number: A48573; MUID:93165070; PMID:8433712
A>Accession: A48573
A>Status: preliminary
A>Molecule type: mRNA
A>Residues: 1-393 <KHA>
A>Cross-references: GB:M93097; NID:G160928
A>Note: sequence inconsistent with the nucleotide translation
A>Note: sequence extracted from NCBI backbone (NCBIN:125085, NCBI:P:125086)
C:Superfamily: calreticulin
F:1-16/Domain: signal sequence #status predicted <SIG>
F:390-393/Region: endoplasmic reticulum retention signal

Query Match 70.5%; Score 182; DB 1; Length 393;
Best Local Similarity 71.4%; Pred. No. 1.1e-14;
Matches 35; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 1 NYKGKWLINKDIRCKDDFFTHLYTLIVRPDNTYEVKIDNSQVSGSLE 49
||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB 147 NYKGKWLIRKKEIPCKDKDLKTHLYTLIVPNPNKYEVLDNAKVEEGSLE 195

RESULT 14
S25851
calreticulin precursor - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 06-Jan-1994 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999
C>Accession: S25851; T33996
R:Smith, M.J
DNA Seq. 2, 235-240, 1992
A>Title: A C. elegans gene encodes a protein homologous to mammalian calreticulin.
A>Reference number: S25851; MUID:92329978; PMID:1162782
A>Accession: S25851
A>Status: preliminary
A>Molecule type: DNA
A>Residues: 1-395 <SMI>
A>Cross-references: EMBL:X59589; NID:G6693; PIDN:CAA42159.1; PID:G6694
R:Bauer, C.; Courtney, L.; Lapiant, Y.
Submitted to the EMBL Data Library, February 1999
A>Description: The sequence of C. elegans cosmid Y38A10A.
A>Reference number: Z21453
A>Accession: T33996
A>Status: preliminary; translated from GB/EMBL/DBJ
A>Molecule type: DNA
A>Residues: 1-395 <BAU>
A>Cross-references: EMBL:AF125963; PIDN:AAI4746.1; GSPDB:GN00023; CESP:Y38A10A.5
A>Experimental source: strain Bristol N2; clone Y38A10A
C>Genetics:
A>Gene: CESP:Y38A10A.5
A>Map position: 5
A>Introns: 107/3; 315/3
C:Superfamily: calreticulin
F:1-15/Domain: signal sequence #status predicted <SIG>
F:392-395/Region: endoplasmic reticulum retention signal

Query Match 69.4%; Score 179; DB 2; Length 395;
Best Local Similarity 67.3%; Pred. No. 2.6e-14;
Matches 33; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 NYKGKWLINKDIRCKDDFFTHLYTLIVRPDNTYEVKIDNSQVSGSLE 49
||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB 144 NYKGKWLIRKKEITCKSDLTHLYTLILNSDNTYEVKIDGESAQTSLE 192

RESULT 15
S58170
calreticulin precursor - maize
C:Species: Zea mays (maize)
C>Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 13-Aug-1999
C>Accession: S58170; S49818
R:Dresselhaus, T.; Hagel, C.; Loerz, H.; Kranz, E.
Submitted to the EMBL Data Library, July 1995

```

A;Description: Isolation of a cDNA encoding Calreticulin from in vitro zygotes of maize.
 A;Reference number: S58170
 A;Accession: S58170
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-421 <DRE>
 A;Cross-references: EMBL:X89813; NID:g927571; PIDN:CAA61939.1; PID:g927572
 R;Napier, R.M.; Trueman, S.; Henderson, J.; Boyce, J.M.; Hawes, C.R.; Fricker, M.D.; Ven
 submitted to the EMBL Data Library, November 1994
 A;Description: Purification and sequencing of calreticulin from maize and evidence for it
 A;Reference number: S49818
 A;Accession: S49818
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-421 <NAP>
 A;Cross-references: EMBL:Z46772; NID:g577611; PIDN:CAA86728.1; PID:g577612
 C;Genetics:
 A;Gene: CRT1
 C;Superfamily: calreticulin
 C;Keywords: calcium binding
 F;1-25/Domain: signal sequence #status predicted <SIG>
 F;418-421/Region: endoplasmic reticulum retention signal

Query Match 57.4%; Score 148; DB 2; Length 421;
 Best Local Similarity 55.8%; Fred. No. 1.8e-10;
 Matches 25; Conservative 10; Mismatches 10; Indels 0; Gaps 0;

QY 4 GKXVLKDKIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSL 48
 Db 158 GKXHLIKKDVPCETDQLTHVYTLIIRPDATYSLIDNEKQTGSI 202

Search completed: October 4, 2004, 13:06:35
 Job time: 11.6647 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 4, 2004, 12:50:22 ; Search time 37.1824 Seconds
(without alignments)
372.349 Million cell updates/sec

Title: US-09-807-148-6

Perfect score: 258
Sequence: 1 NYGKRVNLINKDIRCKDEF.....PNTYEVKIDNSQVSGSLE 49

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Genesep_29Jan04:*
1: Genesep1980s:*
2: Genesep1990s:*
3: Genesep2000s:*
4: Genesep2001s:*
5: Genesep2002s:*
6: Genesep2003as:*
7: Genesep2003bs:*
8: Genesep2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	258	100.0	49	3 AAY92353	Aay92353 Recombina
2	258	100.0	60	3 AAY92354	Aay92354 Recombina
3	258	100.0	61	3 AAY92352	Aay92352 Recombina
4	258	100.0	180	3 AAY92351	Aay92351 Human vas
5	258	100.0	280	3 AAY92355	Aay92355 Recombina
6	258	100.0	400	3 AAY92350	Aay92350 Recombina
7	258	100.0	401	2 AAU11156	AAU11156 Calreticu
8	258	100.0	416	7 ADE56306	Ade56306 Rat Prote
9	258	100.0	416	7 ADE56310	Ade56310 Rat Prote
10	258	100.0	417	1 AAP92276	Aap92276 60 kD Ro
11	258	100.0	417	2 AAY00927	Aay00927 Calreticu
12	258	100.0	417	3 AAY92349	Aay92349 Human MBP
13	258	100.0	417	5 AAU77712	AAU77712 Human cal
14	258	100.0	417	5 AAE24591	Aae24591 Human cal
15	258	100.0	417	5 AAEL1851	Aae1851 Human cal
16	258	100.0	417	5 ABB82384	Abb82384 Human cal
17	258	100.0	417	6 ABJ19766	Abj19766 Human MP2
18	258	100.0	417	6 AAG79824	Aag79824 Calreticu
19	258	100.0	417	6 ADA26337	Ada26337 Human cal
20	258	100.0	417	7 ADD22407	Add22407 HLA-B*6 T
21	258	100.0	417	7 ADE56308	Ade56308 Human Pro
22	258	100.0	417	7 ADE56312	Ade56312 Human Pro
23	218	84.5	403	2 AAU04171	Aau04171 Flea calr
24	209	81.0	406	4 ABB64414	Abb64414 Drosophil
25	190	73.6	122	2 AAY00926	Aay00926 Rat cc1qr

26	190	73.6	122	2 AAY00924	Aay00924 Human cCl
27	182	70.5	122	2 AAY00925	Aay00925 Mouse cCl
28	182	70.5	336	2 AAR12312	Aar12312 Partial s
29	145	56.2	385	3 AAB32385	Aab32385 Human sec
30	145	56.2	390	6 ABO07134	Ab007134 Novel hum
31	144	55.8	419	7 ABM74155	Abm74155 DNA clone
32	143	55.4	415	4 AAB66343	Aab66343 Castor be
33	143	55.4	415	4 AAB66341	Aab66341 Castor be
34	142	55.0	420	5 ABB04656	Abb04656 Maize cal
35	139	53.9	428	7 ABM74288	Abm74288 DNA clone
36	135	52.3	312	3 AAG47933	Aag47933 Arabidops
37	135	52.3	312	3 AAG24609	Aag24609 Arabidops
38	135	52.3	332	3 AAG30998	Aag30998 Arabidops
39	135	52.3	421	3 AAG24608	Aag24608 Arabidops
40	135	52.3	421	3 AAG47932	Aag47932 Arabidops
41	135	52.3	424	3 AAG24607	Aag24607 Arabidops
42	135	52.3	424	3 AAG47931	Aag47931 Arabidops
43	135	52.3	441	3 AAG30997	Aag30997 Arabidops
44	135	52.3	444	3 AAG30996	Aag30996 Arabidops
45	101	39.1	591	4 ABB44553	Abb44553 Mouse wou

ALIGNMENTS

RESULT 1

RAY92353

ID AAY92353 standard; protein; 49 AA.

XX

AC AAY92353;

XX

DT 10-AUG-2000 (first entry)

XX

DE Recombinant human calreticulin residues 132-180.

XX

KW MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;
endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
cytostatic; dermatologic; immunosuppressive; antiinflammatory; hepatic;
anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.

XX

OS Homo sapiens.

OS

CS Synthetic.

XX

PN WC200020577-A1.

XX

PD 13-APR-2000.

XX

PF 05-OCT-1999; 99WO-US023240.

XX

PR 06-OCT-1998; 98US-0103438P.

XX

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX

PI Tosato G, Pike SE, Yao L;

XX

DR WPI; 2000-303767/26.

XX

PT Inhibiting endothelial cell growth and angiogenesis using calreticulin,
useful for suppressing tumor growth.

XX

PS Claim 4; Page 82-83; 99pp; English.

XX

CC A novel method of inhibiting endothelial cell growth comprises contacting
the cells with calreticulin (or its fragments/variants). Fragments of
calreticulin causes at least 40% inhibition of angiogenesis, tumor growth
and/or endothelial cell growth (claimed). The method may be used for
inhibiting angiogenesis in a patient. The angiogenesis is associated with
a disease other than a tumor that is associated with neovascularization
(e.g. diabetic neuropathy, retrolental fibroplasia, trachoma, neovascular
glaucoma, psoriasis, angiofibrosis, immune inflammation,
atherosclerosis, excessive wound repair, retinal neovascularization,
macular degeneration, corneal graft rejection, contact lens overwear,
Crohn's disease, non-immune inflammation, rheumatoid arthritis, systemic

CC lupus erythematosus, thyroiditis, Goodpasture's syndrome, systemic
 CC vasculitis, scleroderma, Sjorgen's syndrome, sarcoidosis and primary
 CC biliary cirrhosis). The method may also be used for treating/inhibiting
 CC tumor growth especially Kaposi's sarcoma (claimed)
 XX
 SQ Sequence 49 AA;

Query Match 100.0%; Score 258; DB 3; Length 49;
 Best Local Similarity 100.0%; Pred. No. 3.4e-31;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSLE 49
 Db 1 NYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSLE 49

RESULT 2

AA92354
 ID AAY92354 standard; protein; 60 AA.

AC AAY92354;

DT 10-AUG-2000 (first entry)

DE Recombinant human calreticulin residues 121-180.

KW MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;
 KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
 KW cytostatic; dermatological; immunosuppressive; antiinflammatory; hepatic;
 KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.

OS Homo sapiens.

OS Synthetic.

PN WO200020577-A1.

PD 13-APR-2000.

PF 05-OCT-1999; 99WO-US023240.

PR 06-OCT-1998; 98US-0103438P.

PS (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Tosato G, Pike SE, Yao L;

DR WPI; 2000-303767/26.

XX Inhibiting endothelial cell growth and angiogenesis using calreticulin,
 PT useful for suppressing tumor growth.

PS Claim 4; Page 85; 99pp; English.

CC A novel method of inhibiting endothelial cell growth comprises contacting
 CC the cells with calreticulin (or its fragments/variants). Fragments of
 CC calreticulin causes at least 40% inhibition of angiogenesis, tumor growth
 CC and/or endothelial cell growth (claimed). The method may be used for
 CC inhibiting angiogenesis in a patient. The angiogenesis is associated with
 CC a disease other than a tumor that is associated with neovascularization
 CC (e.g. diabetic neuropathy, retrolental fibroplasia, trachoma, neovascular
 CC glaucoma, psoriasis, angiofibromas, immune inflammation,
 CC atherosclerosis, excessive wound repair, retinal neovascularization,
 CC macular degeneration, corneal graft rejection, contact lens overwear,
 CC Crohn's disease, non-immune inflammation, rheumatoid arthritis, systemic
 CC lupus erythematosus, thyroiditis, Goodpasture's syndrome, systemic
 CC vasculitis, scleroderma, Sjorgen's syndrome, sarcoidosis and primary
 CC biliary cirrhosis). The method may also be used for treating/inhibiting
 CC tumor growth especially Kaposi's sarcoma (claimed)

XX Sequence 60 AA;

Query Match 100.0%; Score 258; DB 3; Length 60;
 Best Local Similarity 100.0%; Pred. No. 4.4e-31;

Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSLE 49
 Db 12 NYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSLE 60

RESULT 3

AA92352
 ID AAY92352 standard; protein; 61 AA.

AC AAY92352;

DT 10-AUG-2000 (first entry)

DE Recombinant human calreticulin residues 120-180.

KW MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;
 KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
 KW cytostatic; dermatological; immunosuppressive; antiinflammatory; hepatic;
 KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.

OS Homo sapiens.

OS Synthetic.

PN WO200020577-A1.

PD 13-APR-2000.

PF 05-OCT-1999; 99WO-US023240.

PR 06-OCT-1998; 98US-0103438P.

PS (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Tosato G, Pike SE, Yao L;

DR WPI; 2000-303767/26.

XX Inhibiting endothelial cell growth and angiogenesis using calreticulin,
 PT useful for suppressing tumor growth.

PS Claim 4; Page 82-83; 99pp; English.

CC A novel method of inhibiting endothelial cell growth comprises contacting
 CC the cells with calreticulin (or its fragments/variants). Fragments of
 CC calreticulin causes at least 40% inhibition of angiogenesis, tumor growth
 CC and/or endothelial cell growth (claimed). The method may be used for
 CC inhibiting angiogenesis in a patient. The angiogenesis is associated with
 CC a disease other than a tumor that is associated with neovascularization
 CC (e.g. diabetic neuropathy, retrolental fibroplasia, trachoma, neovascular
 CC glaucoma, psoriasis, angiofibromas, immune inflammation,
 CC atherosclerosis, excessive wound repair, retinal neovascularization,
 CC macular degeneration, corneal graft rejection, contact lens overwear,
 CC Crohn's disease, non-immune inflammation, rheumatoid arthritis, systemic
 CC lupus erythematosus, thyroiditis, Goodpasture's syndrome, systemic
 CC vasculitis, scleroderma, Sjorgen's syndrome, sarcoidosis and primary
 CC biliary cirrhosis). The method may also be used for treating/inhibiting
 CC tumor growth especially Kaposi's sarcoma (claimed)

XX Sequence 61 AA;

Query Match 100.0%; Score 258; DB 3; Length 61;
 Best Local Similarity 100.0%; Pred. No. 4.5e-31;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSLE 49
 Db 13 NYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSLE 61

RESULT 4

AA92351

ID AAY92351 standard; protein; 180 AA.
 AC AAY92351;
 XX
 DT 10-AUG-2000 (first entry)
 XX
 DE Human vasostatin (calreticulin N-terminal 180 amino acids).
 XX
 XX MBP-calreticulin; maltose binding protein; vasostatin; N-terminal;
 KW angiogenesis; inhibition; endothelial cell; anti-angiogenic;
 KW neuroprotective; antidiabetic; cytostatic; dermatological; hepatic;
 KW immunosuppressive; anti-inflammatory; anti-atherosclerotic;
 KW gastrointestinal; anti-arthritis; ophthalmic.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX WO200020577-A1.
 PN
 XX 13-APR-2000.
 PD
 XX 05-OCT-1999; 99WO-US023240.
 PF
 XX 06-OCT-1998; 98US-0103438P.
 PR
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA
 XX Tosato G, Pike SE, Yao L;
 PI WPI; 2000-303767/26.
 XX
 XX Inhibiting endothelial cell growth and angiogenesis using calreticulin,
 PT useful for suppressing tumor growth.
 XX
 PS Claim 4; Page 82; 99pp; English.
 XX
 XX A novel method of inhibiting endothelial cell growth comprises contacting
 CC the cells with calreticulin (or its fragments/variants). Fragments of
 CC calreticulin causes at least 40% inhibition of angiogenesis, tumor growth
 CC and/or endothelial cell growth (claimed). The method may be used for
 CC inhibiting angiogenesis in a patient. The angiogenesis is associated with
 CC a disease other than a tumor that is associated with neovascularization
 CC (e.g. diabetic neuropathy, retrolental fibroplasia, trachoma, neovascular
 CC glaucoma, psoriasis, angiofibromas, immune inflammation,
 CC atherosclerosis, excessive wound repair, retinal neovascularization,
 CC macular degeneration, corneal graft rejection, contact lens overwear,
 CC Crohn's disease, non-immune inflammation, rheumatoid arthritis, systemic
 CC lupus erythematosus, thyroiditis, Goodpasture's syndrome, systemic
 CC vasculitis, scleroderma, Sjorgen's syndrome, sarcoidosis and primary
 CC biliary cirrhosis). The method may also be used for treating/inhibiting
 CC tumor growth especially Kaposi's sarcoma (claimed)
 XX
 SQ Sequence 180 AA;
 Query Match 100.0%; Score 258; DB 3; Length 180;
 Best Local Similarity 100.0%; Pred. No. 1.9e-30;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 NYKGNVLNKKDKDETHLYTLVLRPNTYEVKIDNSQVESGSL 49
 Db 132 NYKGNVLNKKDKDETHLYTLVLRPNTYEVKIDNSQVESGSL 180
 RESULT 5
 AAY92355
 ID AAY92355 standard; protein; 280 AA.
 XX
 AC AAY92355;
 XX
 DT 10-AUG-2000 (first entry)
 XX
 DE Recombinant delta-120 calreticulin.
 XX

KW MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;
 KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
 KW cytostatic; dermatological; immunosuppressive; anti-inflammatory; hepatic;
 XX anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.
 OS Homo sapiens.
 OS Synthetic.
 XX WO200020577-A1.
 PN
 XX 13-APR-2000.
 PD
 XX 05-OCT-1999; 99WO-US023240.
 PF
 XX 06-OCT-1998; 98US-0103438P.
 PR
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA
 XX Tosato G, Pike SE, Yao L;
 PI WPI; 2000-303767/26.
 XX
 XX Inhibiting endothelial cell growth and angiogenesis using calreticulin,
 PT useful for suppressing tumor growth.
 XX
 PS Claim 4; Page 86; 99pp; English.
 XX
 XX This sequence comprises recombinant human calreticulin (AAY92350) missing
 CC the N-terminal 120 amino acids. A novel method of inhibiting endothelial
 CC cell growth comprises contacting the cells with calreticulin (or its
 CC fragments/variants). Fragments of calreticulin causes at least 40%
 CC inhibition of angiogenesis, tumor growth and/or endothelial cell growth
 CC (claimed). The method may be used for inhibiting angiogenesis in a
 CC patient. The angiogenesis is associated with a disease other than a tumor
 CC that is associated with neovascularization (e.g. diabetic neuropathy,
 CC retrolental fibroplasia, trachoma, neovascular glaucoma, psoriasis,
 CC angiofibromas, immune inflammation, atherosclerosis, excessive wound
 CC repair, retinal neovascularization, macular degeneration, corneal graft
 CC rejection, contact lens overwear, Crohn's disease, non-immune
 CC inflammation, rheumatoid arthritis, systemic lupus erythematosus,
 CC thyroiditis, Goodpasture's syndrome, systemic vasculitis, scleroderma,
 CC Sjorgen's syndrome, sarcoidosis and primary biliary cirrhosis). The
 CC method may also be used for treating/inhibiting tumor growth especially
 CC Kaposi's sarcoma (claimed)
 XX
 SQ Sequence 280 AA;
 Query Match 100.0%; Score 258; DB 3; Length 280;
 Best Local Similarity 100.0%; Pred. No. 3.4e-30;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 NYKGNVLNKKDKDETHLYTLVLRPNTYEVKIDNSQVESGSL 49
 Db 12 NYKGNVLNKKDKDETHLYTLVLRPNTYEVKIDNSQVESGSL 60
 RESULT 6
 AAY92350
 ID AAY92350 standard; protein; 400 AA.
 XX
 AC AAY92350;
 XX
 DT 10-AUG-2000 (first entry)
 XX
 DE Recombinant human MBP-calreticulin.
 XX
 KW MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;
 KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
 KW cytostatic; dermatological; immunosuppressive; anti-inflammatory; hepatic;
 KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.
 XX
 OS Homo sapiens.
 OS

```
PN WO200020577-A1.
XX
XX
PD 13-APR-2000.
XX
XX 05-OCT-1999; 99WO-US023240.
XX
XX 06-OCT-1998; 98US-0103438P.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Tosato G, Pike SE, Yao L;
PI
XX WPI; 2000-303767/26.
DR
XX N-PSDB; AAA09346, AAA09347.
XX
XX Inhibiting endothelial cell growth and angiogenesis using calreticulin,
PT useful for suppressing tumor growth.
XX
XX Claim 4; Page 80-81; 99pp; English.
XX
XX Recombinant human MBP-calreticulin comprises the sequence of human
XX calreticulin (see AAY92349) without the 17 N-terminal amino acids. A
XX novel method of inhibiting endothelial cell growth comprises contacting
XX the cells with calreticulin (or its fragments/variants). Fragments of
XX calreticulin causes at least 40% inhibition of angiogenesis, tumor growth
XX and/or endothelial cell growth (claimed). The method may be used for
XX inhibiting angiogenesis in a patient. The angiogenesis is associated with
XX a disease other than a tumor that is associated with neovascularization
XX (e.g. diabetic neuropathy, retrolental fibroplasia, trachoma, neovascular
XX glaucoma, psoriasis, angiodermas, immune inflammation,
XX atherosclerosis, excessive wound repair, retinal neovascularization,
XX macular degeneration, corneal graft rejection, contact lens overwear,
XX Crohn's disease, non-immune inflammation, rheumatoid arthritis, systemic
XX lupus erythromatosus, thyroiditis, Goodpasture's syndrome, systemic
XX vasculitis, scleroderma, Sjorgen's syndrome, sarcoidosis and primary
XX biliary cirrhosis). The method may also be used for treating/inhibiting
XX tumor growth especially Kaposi's sarcoma (claimed)
XX
XX Sequence 400 AA;

Query Match 100.0%; Score 258; DB 3; Length 400;
Best Local Similarity 100.0%; Pred. No. 5.4e-30;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSLE 49
Db 132 NYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSLE 180

RESULT 7
AAW11156
ID AAW11156 standard; peptide; 401 AA.
XX
XX AAW11156;
XX
XX 31-MAY-1997 (first entry)
XX
XX Calreticulin.
DE
XX
XX calreticulin; C-domain; restenosis; inhibitor.
KW
XX
XX Homo sapiens.
OS
XX
XX WO9636643-A1.
PN
XX
XX 21-NOV-1996.
PD
XX
XX 17-MAY-1996; 96WO-IB000471.
PF
XX
XX 17-MAY-1995; 95US-00442844.
PR
XX
XX 16-MAY-1996; 95US-00649417.
XX
XX (UTAL-) UNIV ALBERTA.
PA

Query Match 100.0%; Score 258; DB 2; Length 401;
Best Local Similarity 100.0%; Pred. No. 5.4e-30;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSLE 49
Db 132 NYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSLE 180

RESULT 8
ADE56306
ID ADE56306 standard; protein; 416 AA.
XX
XX ADE56306;
XX
XX 29-JAN-2004 (first entry)
XX
XX Rat Protein P18418, SEQ ID NO 2158.
DE
XX
XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
XX chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
KW
XX
XX Rattus norvegicus.
OS
XX
XX WO2003016475-A2.
PN
XX
XX 27-FEB-2003.
PD
XX
XX 14-AUG-2002; 2002WO-US025765.
PF
XX
XX 14-AUG-2001; 2001US-0312147P.
PR
XX
XX 01-NOV-2001; 2001US-0346382P.
PR
XX
XX 26-NOV-2001; 2001US-0333347P.
XX
XX (GEHO ) GEN HOSPITAL CORP.
PA
XX
XX (FARB ) BAYER AG.
XX
XX Woolf C, D'urso D, Befort K, Costigan M;
PI
XX
XX WPI; 2003-268312/26.
DR
XX
XX GENBANK; P18418.
XX
XX New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
XX Claim 1; Page; 1017pp; English.
XX
XX The invention discloses a composition comprising two or more isolated rat
XX or human polynucleotides or a polynucleotide which represents a fragment,
XX derivative or allelic variation of the nucleic acid sequence. Also
XX claimed are a vector comprising the novel polynucleotide, a host cell
XX comprising the vector, a method for identifying a nucleotide sequence
XX which is differentially regulated in an animal subjected to pain and a
XX kit to perform the method, an array, a method for identifying an agent
XX that increases or decreases the expression of the polynucleotide sequence
```

CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 416 AA;

SQ Query Match 100.0%; Score 258; DB 7; Length 416;
 Best Local Similarity 100.0%; Pred. No. 5,7e-30;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYKGNVLINKDIRCKDETHLYTLVRPDNTYEVKIDNSQVESGSLE 49
 Db 149 NYKGNVLINKDIRCKDETHLYTLVRPDNTYEVKIDNSQVESGSLE 197

RESULT 9

AD56310 ID ADE56310 standard; protein; 416 AA.

XX AC ADE56310;

XX DT 29-JAN-2004 (first entry)

XX DE Rat Protein P18418, SEQ ID NO 2162.

XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
 KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

XX OS Rattus norvegicus.

XX PN WO2003016475-A2.

XX PD 27-FEB-2003.

XX PF 14-AUG-2002; 2002WO-US025765.

XX PR 14-AUG-2001; 2001US-0312147P.

XX PR 01-NOV-2001; 2001US-0346382P.

XX PR 26-NOV-2001; 2001US-0333347P.

XX PA (GEHO) GEN HOSPITAL CORP.

XX PA (FARB) BAYER AG.

XX PI Woolf C, D'urso D, Befort K, Costigan M;

XX DR WPI; 2003-268312/26.

XX DR GENBANK; F18418.

XX New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.

XX PS Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell

CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 416 AA;

SQ Query Match 100.0%; Score 258; DB 7; Length 416;
 Best Local Similarity 100.0%; Pred. No. 5,7e-30;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYKGNVLINKDIRCKDETHLYTLVRPDNTYEVKIDNSQVESGSLE 49
 Db 149 NYKGNVLINKDIRCKDETHLYTLVRPDNTYEVKIDNSQVESGSLE 197

RESULT 10

AAP2276 ID AAP2276 standard; protein; 417 AA.

XX AC AAP2276;

XX DT 25-MAR-2003 (revised)

XX DT 23-FEB-1990 (first entry)

XX DE 60 kD Ro (Ro/SSA) antigen.

XX KW Sjorens syndrome; systemic lupus erythematosus.

XX OS Synthetic.

XX PN WO8909273-A.

XX PD 05-OCT-1989.

XX PF 22-MAR-1989; 89WO-US001213.

XX PR 22-MAR-1988; 88US-00171634.

XX PA (TEXA) UNIV TEXAS SYSTEM.

XX PI Sontheimer RD, Lieu TS, Capra JD, Mccaulliffe DP;

XX DR WPI; 1989-309537/42.

XX DR N-PSDB; AAP2276.

XX DNA sequences encoding antigenic epitope(s) of RO 60 kD auto-antigen -
 PT used in immunoassays to detect rheumatic disease.

XX PS Disclosure; Fig 2; 88pp; English.

XX Synthetic peptides corresp. to an epitopic core of Ro antigen are
 CC expressed recombinantly to detect autoantibodies, for identification of
 CC autoimmune diseases. These epitopes are AAS 24-36, 23-36, 188-209, or 241

CC -255. The peptides may be substd. for ribonucleoprotein particle
 CC antigens. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-
 CC MAR-2003 to correct PI field.)
 XX
 SQ Sequence 417 AA;

Query Match 100.0%; Score 258; DB 1; Length 417;
 Best Local Similarity 100.0%; Pred. No. 5.7e-30;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYKGNVLINKIRCKDDFTHTLYTLIVRPDNTYEVKIDNSQVSGSLE 49
 DB 149 NYKGNVLINKIRCKDDFTHTLYTLIVRPDNTYEVKIDNSQVSGSLE 197

RESULT 11

AAV00927
 ID AAY00927 standard; protein; 417 AA.

XX AC AAY00927;

XX DT 28-MAY-1999 (first entry)

XX DE Calreticulin.

XX KW C1q and collectin receptor; cC1qR binding domain; complement ubiquitin;
 KW CUB functionality; inhibitor; complement activation; inflammation;
 KW myocardial infarction; brain ischaemia; gut ischaemia; amyloid plaque;
 KW rheumatoid arthritis; systemic lupus erythematosus; Alzheimer's disease;
 KW immune complex nephritis; therapy.

XX OS Homo sapiens.

XX FN WO9907406-A1.

XX PD 18-FEB-1999.

XX PF 12-AUG-1998; 98WO-GE02430.

XX PR 12-AUG-1997; 97GB-00016998.

XX PA (UYLE-) UNIV LEICESTER.

XX PI Schwaebler W;

XX DR WPI; 1999-180404/15.

XX PT Use of a cC1qR binding domain - to modulate complement ubiquitin (CUB)
 XX functionality.

XX PS Disclosure; Page 26-27; 31pp; English.

XX CC This sequence is calreticulin, a homologue of C1q and collectin receptor
 CC (cC1qR). The invention relates to the use of a cC1qR binding domain in a
 CC medicament to effect complement ubiquitin (CUB) functionality, and an
 CC inhibitor of the cC1qR binding domain in a medicament to inhibit CUB
 CC functionality. The cC1qR binding domain, or its inhibitor, can be used to
 CC treat a human or animal body. Particularly an inhibitor is used to treat
 CC complement activation involved in the initiation and maintenance of
 CC inflammation, for example in myocardial infarction, brain ischaemia
 CC (stroke), gut ischaemia, rheumatoid arthritis, systemic lupus
 CC erythematosus, burns, immune complex nephritis, and to treat amyloid
 CC plaques in Alzheimer's disease. The use of cC1qR binding domain or
 CC inhibitor enables the CUB domain functionality to be modulated using a
 CC low molecular weight molecule

XX SQ Sequence 417 AA;

Query Match 100.0%; Score 258; DB 2; Length 417;
 Best Local Similarity 100.0%; Pred. No. 5.7e-30;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYKGNVLINKIRCKDDFTHTLYTLIVRPDNTYEVKIDNSQVSGSLE 49

DB 149 NYKGNVLINKIRCKDDFTHTLYTLIVRPDNTYEVKIDNSQVSGSLE 197

RESULT 12

AAV92349

ID AAY92349 standard; protein; 417 AA.

XX AC AAY92349;

XX DT 10-AUG-2000 (first entry)

XX DE Human MBP-calreticulin.

XX KW MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;
 KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
 KW cytoskeletal; dermalogical; immunosuppressive; anti-inflammatory; hepatic;
 KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Peptide 1..17

FT Protein /label= signal_peptide

FT Protein 18

FT Protein /label= mature_protein

XX PN WO200020577-A1.

XX PD 13-APR-2000.

XX PF 05-OCT-1999; 99WO-US023240.

XX PR 06-OCT-1998; 98US-0103438P.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PI Tosato G, Pike SE, Yao L;

XX DR WPI; 2000-303767/26.

XX DR N-PSDB; AAA09346, AAA09347.

XX PT Inhibiting endothelial cell growth and angiogenesis using calreticulin,
 XX useful for suppressing tumor growth.

XX PS Disclosure; Page 79-80; 99pp; English.

XX CC A novel method of inhibiting endothelial cell growth comprises contacting
 CC the cells with calreticulin (or its fragments/variants). Fragments of
 CC calreticulin causes at least 40% inhibition of angiogenesis, tumor growth
 CC and/or endothelial cell growth (claimed). The method may be used for
 CC inhibiting angiogenesis in a patient. The angiogenesis is associated with
 CC a disease other than a tumor that is associated with neovascularization
 CC (e.g. diabetic neuropathy, retrolental fibroplasia, trachoma, neovascular
 CC glaucoma, psoriasis, angioblastomas, immune inflammation,
 CC atherosclerosis, excessive wound repair, retinal neovascularization,
 CC macular degeneration, corneal graft rejection, contact lens overwear,
 CC Crohn's disease, non-immune inflammation, rheumatoid arthritis, systemic
 CC lupus erythematosus, thyroiditis, Goodpasture's syndrome, systemic
 CC vasculitis, scleroderma, Sjorgen's syndrome, sarcoidosis and primary
 CC biliary cirrhosis). The method may also be used for treating/inhibiting
 CC tumor growth especially Kaposi's sarcoma (claimed)

XX SQ Sequence 417 AA;

Query Match 100.0%; Score 258; DB 3; Length 417;
 Best Local Similarity 100.0%; Pred. No. 5.7e-30;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYKGNVLINKIRCKDDFTHTLYTLIVRPDNTYEVKIDNSQVSGSLE 49

DB 149 NYKGNVLINKIRCKDDFTHTLYTLIVRPDNTYEVKIDNSQVSGSLE 197

FT Domain /label= Alpha_helix
 FT 171..285
 FT /note= "Proline-rich domain (P domain)"
 FT 286..397
 FT /label= C-terminal_domain

XX WO200206327-A2.

XX 24-JAN-2002.

XX 17-JUL-2001; 2001WO-US022357.

XX 17-JUL-2000; 2000US-0218761P.

XX 16-JUL-2001; 2001US-00906393.

XX (NOUN) UNIV NORTHWESTERN.

XX Wang Z, Xiao W;

XX WPI; 2002-179780/23.

XX N-PSDB; AAD29931.

XX Identifying a subject that is likely to have aggressive form of prostate cancer, involves comparing calreticulin levels in prostate specimen of the subject and in benign prostatic epithelial cells of the same subject.

PS Disclosure; Page 146-148; 148pp; English.

XX The present invention relates to methods of distinguishing aggressive forms of prostate cancer from non-aggressive forms. The method involves comparing the level of calreticulin in prostate specimen and in benign prostatic epithelial cells of a subject. The invention particularly relates to two proteins, namely calreticulin and T1D-1 (TRAITS; U19) that are down-regulated in aggressive forms of prostate cancer but not in slowly progressing prostate cancer. They play important roles in the part of androgen action pathway that suppresses cell proliferation and/or prevents prostate cancer. The method is useful for identifying a subject who is likely to have an aggressive form of prostate cancer. The invention further relates to a method of identifying a subject with a slow growing form of prostate cancer. T1D-1 sequences are useful for treating cancers such as epithelium-derived carcinomas, kidney cancers, lymphomas, leukaemias and prostate cancers. Sequences of the invention are used as vaccines and in gene therapy. The present sequence is human calreticulin protein

XX Sequence 417 AA;

Query Match 100.0%; Score 258; DB 5; Length 417;
 Best Local Similarity 100.0%; Pred. No. 5.7e-30;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYKGNVLINKDIRCKDDEFTLYLIVRPNTYEVKIDNSQVSGSLE 49

Db 149 NYKGNVLINKDIRCKDDEFTLYLIVRPNTYEVKIDNSQVSGSLE 197

Search completed: October 4, 2004, 13:03:31
 Job time : 37.1824 secs

Sequence 4, Appli
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Sequence 41, Appl
Sequence 41, Appl
Sequence 8, Appli
Sequence 8, Appli
Sequence 4469, Ap
Sequence 3, Appli
Sequence 3, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 15, Appli
Sequence 15, Appli
Sequence 5080, Ap
Sequence 13, Appl
Sequence 7, Appli
Sequence 54, Appl
Sequence 54, Appl
Sequence 54, Appl

US-09-784-508-4
US-09-328-352-7004
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US-08-237-401A-41
US-09-700-397-8
US-09-134-001C-4469
US-08-752-238-3
US-09-085-603B-3
US-09-031-897-7
US-03-257-770-6
US-08-336-447A-15
US-09-091-117-2
US-09-134-001C-5080
US-08-483-101-13
US-08-419-652-7
US-08-190-802A-54
US-08-477-346-54
US-08-473-089-54

28 52.5 20.3 358 4
29 52 20.2 116 4
30 51.5 20.0 54 2
31 51.5 20.0 54 2
32 51 19.8 478 4
33 50.5 19.6 513 4
34 50.5 19.6 599 1
35 50.5 19.6 599 3
36 50.5 19.6 599 3
37 50.5 19.6 599 4
38 50 19.4 889 4
39 50 19.4 1030 3
40 50 19.4 3696 4
41 49.5 19.2 238 2
42 49.5 19.2 620 2
43 49.5 19.2 816 1
44 49.5 19.2 816 3
45 49.5 19.2 816 4

US-09-828-000-8
; Sequence 8, Application US/09828000
; Patent No. 6596690
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/09/828,000
; CURRENT FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Fragment 5
US-09-828-000-8

Query Match 100.0%; Score 258; DB 4; Length 61;
Best Local Similarity 100.0%; Pred. No. 3.2e-30;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYKGNVLINKIRCKDEFFHLYTLIVRPDNTYEVKIDNSQVESGSLE 49
Db 13 NYKGNVLINKIRCKDEFFHLYTLIVRPDNTYEVKIDNSQVESGSLE 61

RESULT 2
US-09-828-000-3
; Sequence 3, Application US/09828000
; Patent No. 6596690
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/09/828,000
; CURRENT FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Vasostatin
US-09-828-000-3

Query Match 100.0%; Score 258; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.3e-29;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYKGNVLINKIRCKDEFFHLYTLIVRPDNTYEVKIDNSQVESGSLE 49

ALIGNMENTS

RESULT 1

US-09-828-000-8
; Sequence 8, Application US/09828000
; Patent No. 6596690
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/09/828,000
; CURRENT FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Fragment 5
US-09-828-000-8

Query Match 100.0%; Score 258; DB 4; Length 61;
Best Local Similarity 100.0%; Pred. No. 3.2e-30;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYKGNVLINKIRCKDEFFHLYTLIVRPDNTYEVKIDNSQVESGSLE 49
Db 13 NYKGNVLINKIRCKDEFFHLYTLIVRPDNTYEVKIDNSQVESGSLE 61

RESULT 2

US-09-828-000-3
; Sequence 3, Application US/09828000
; Patent No. 6596690
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/09/828,000
; CURRENT FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Vasostatin
US-09-828-000-3

Query Match 100.0%; Score 258; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.3e-29;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYKGNVLINKIRCKDEFFHLYTLIVRPDNTYEVKIDNSQVESGSLE 49

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 4, 2004, 13:01:22 ; Search time 10.9529 Seconds
(without alignments)
230.958 Million cell updates/sec

Title: US-09-807-148-6
Sequence: 1 NYKGNVLINKIRCKDEFF.....PNTYEVKIDNSQVESGSLE 49

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	258	100.0	61	4	US-09-828-000-8
2	258	100.0	180	4	US-09-828-000-3
3	258	100.0	416	4	US-09-828-000-2
4	175	67.8	35	4	US-09-828-000-7
5	175	67.8	61	4	US-09-828-000-4
6	143	55.4	415	3	US-08-675-816-2
7	100	38.8	593	1	US-08-296-362-2
8	95	36.8	610	4	US-09-976-594-947
9	82	31.8	18	4	US-09-828-000-6
10	82	31.8	27	4	US-09-828-000-5
11	68	26.4	542	3	US-08-675-816-6
12	61.5	23.8	582	3	US-08-906-865-3
13	61.5	23.8	582	4	US-09-129-668-3
14	55	21.3	588	4	US-09-252-991A-18861
15	54	20.9	405	1	US-07-829-954-2
16	54	20.9	405	1	US-07-994-423-2
17	54	20.9	405	1	US-08-421-891-2
18	53.5	20.7	279	4	US-08-701-191A-23
19	53.5	20.7	279	4	US-09-664-526-23
20	53.5	20.7	355	1	US-08-292-549-6
21	53.5	20.7	355	3	US-09-006-353A-14
22	53.5	20.7	355	4	US-09-573-986-14
23	53.5	20.7	943	4	US-09-540-236-3458
24	53.5	20.7	984	2	US-08-673-789-9
25	53.5	20.7	984	2	US-08-449-645A-19
26	53.5	20.7	984	2	US-08-702-367A-19
27	53.5	20.7	984	5	PCT-US95-04681-19

Db 132 NYKGNVLINKDIRCKDDEFTHTLTVLRPDNTYEVKIDNSQVSGSLE 180
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RESULT 3
US-09-828-000-2
; Sequence 2, Application US/09828000
; Patent No. 6596690
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/09/828,000
; CURRENT FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Calreticulin
US-09-828-000-2

Query Match 100.0%; Score 258; DB 4; Length 416;
Best Local Similarity 100.0%; Pred. No. 3.8e-29;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYKGNVLINKDIRCKDDEFTHTLTVLRPDNTYEVKIDNSQVSGSLE 49
Db 149 NYKGNVLINKDIRCKDDEFTHTLTVLRPDNTYEVKIDNSQVSGSLE 197
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RESULT 4
US-09-828-000-7
; Sequence 7, Application US/09828000
; Patent No. 6596690
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/09/828,000
; CURRENT FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 7
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Fragment 4
US-09-828-000-7

Query Match 67.8%; Score 175; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.7e-18;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYKGNVLINKDIRCKDDEFTHTLTVLRPDN 32
Db 4 NYKGNVLINKDIRCKDDEFTHTLTVLRPDN 35
|||||

RESULT 5
US-09-828-000-4
; Sequence 4, Application US/09828000
; Patent No. 6596690
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/09/828,000
; CURRENT FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 4
; LENGTH: 61
; TYPE: PRT

; ORGANISM: Fragment 1
US-09-828-000-4

Query Match 67.8%; Score 175; DB 4; Length 61;
Best Local Similarity 100.0%; Pred. No. 3.5e-18;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYKGNVLINKDIRCKDDEFTHTLTVLRPDN 32
Db 30 NYKGNVLINKDIRCKDDEFTHTLTVLRPDN 61
|||||

RESULT 6
US-08-675-816-2
; Sequence 2, Application US/08675816
; Patent No. 6171864
; GENERAL INFORMATION:
; APPLICANT: Coughlan, Sean J.
; APPLICANT: Winfrey, Jr., Ron J.
; TITLE OF INVENTION: CALRETICULIN AND CALNEXIN GENES AND PROMOTER REGIONS AND USES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 701 Fifth Ave. Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/675,816
; FILING DATE: 05-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6171864tenburg, Carol
; REGISTRATION NUMBER: 39,317
; REFERENCE/DOCKET NUMBER: 750027.401
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)-622-4900
; TELEFAX: (206)-682-6031
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 415 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-675-816-2

Query Match 55.4%; Score 143; DB 3; Length 415;
Best Local Similarity 50.0%; Pred. No. 1.8e-12;
Matches 24; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

QY 1 NYKGNVLINKDIRCKDDEFTHTLTVLRPDNTYEVKIDNSQVSGSL 48
Db 150 NYNDTHLIKKEVPCETDQTHVYTLVIRPDATYSILIDNVEKQTGSL 197
|||||

RESULT 7
US-08-296-362-2
; Sequence 2, Application US/08296362
; Patent No. 5691306
; GENERAL INFORMATION:
; APPLICANT: Bergeron, John J.M.
; APPLICANT: Thomas, David Y.
; APPLICANT: Wada, Ikuo
; TITLE OF INVENTION: METHODS OF DETECTION AND TREATMENT OF
; TITLE OF INVENTION: PROTEIN TRAPPING DISORDERS AND INCREASING SECRETORY
; TITLE OF INVENTION: PROTEIN PRODUCTION
; NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/296,362
FILING DATE: 25-AUG-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Deshr, Marya S.
REGISTRATION NUMBER: 37,120
REFERENCE/DOCKET NUMBER: 690066.401C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
TELEX: 3723836
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 593 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-296-362-2
Query Match 38.8%; Score 100; DB 1; Length 593;
Best Local Similarity 58.1%; Pred. No. 5e-06; 7; Mismatches 6; Indels 0; Gaps 0;
Matches 18; Conservative 7;
QY 18 DEPTHLYTLIVRPNTVEVKIDNSQVSGSL 48
:|||||:|||||:|||||:|||||:|||||:
DB 233 DKKTHLYTLVNPDSFEILVDQIVNSGNL 263
:|||||:|||||:|||||:|||||:|||||:
RESULT 8
US-09-976-594-947
; Sequence 947, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 947
; LENGTH: 610
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 3876162CD1
US-09-976-594-947
Query Match 36.8%; Score 95; DB 4; Length 610;
Best Local Similarity 54.8%; Pred. No. 2.9e-05;
Matches 17; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
QY 18 DEPTHLYTLIVRPNTVEVKIDNSQVSGSL 48
:|||||:|||||:|||||:|||||:|||||:
DB 223 DRKTHLYTLVNPDDTFEVLVDQIVNKGSL 253
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RESULT 9
US-09-828-000-6
; Sequence 6, Application US/09828000
; Patent No. 6596690
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vastostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/09/828,000
; CURRENT FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Fragment 2
US-09-828-000-6
Query Match 31.8%; Score 82; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NYKGKNVLINKDIRC 15
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DB 4 NYKGKNVLINKDIRC 18
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RESULT 10
US-09-828-000-5
; Sequence 5, Application US/09828000
; Patent No. 6596690
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vastostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/09/828,000
; CURRENT FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Fragment 2
US-09-828-000-5
Query Match 31.8%; Score 82; DB 4; Length 27;
Best Local Similarity 100.0%; Pred. No. 3.8e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NYKGKNVLINKDIRC 15
:|||||:|||||:|||||:|||||:|||||:
DB 13 NYKGKNVLINKDIRC 27
:|||||:|||||:|||||:|||||:|||||:
RESULT 11
US-08-675-816-6
; Sequence 6, Application US/08675816
; Patent No. 6171864
; GENERAL INFORMATION:
; APPLICANT: Coughlan, Sean J.
; APPLICANT: Winfrey, Jr., Ron J.
; TITLE OF INVENTION: CALRETICULIN AND CALNEXIN GENES AND PROMOTER REGIONS AND USES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 701 Fifth Ave. Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/675,816
FILING DATE: 05-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 6171864tenburg, Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 750027.401
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)-622-4900
TELEFAX: (206)-682-6031
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 542 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-675-816-6

Query Match 26.4%; Score 68; DB 3; Length 542;
Best Local Similarity 40.0%; Pred. No. 0.2;
Matches 10; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 18 DEPTHLYLVPRDNTYEVKINSQ 42
DB 181 DKLTHVITALLRPDNLRLVDGE 205

RESULT 12
US-08-906-865-3
Sequence 3, Application US/08906865
Patent No. 6040168
GENERAL INFORMATION:
APPLICANT: Greengard, Paul
APPLICANT: Porton, Barbara
APPLICANT: Kao, Hung-Teh
TITLE OF INVENTION: DNA ENCODING THE HUMAN SYNAPSIN III GENE
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/906,865
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 582 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

DESCRIPTION: /desc = "Synapsin Ila"
HYPOTHEtical: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-906-865-3

Query Match 23.8%; Score 61.5; DB 3; Length 582;
Best Local Similarity 40.0%; Pred. No. 1.9;
Matches 14; Conservative 7; Mismatches 13; Indels 1; Gaps 1;

QY 2 YGKQNVLINKDIRCKDDETHLYTLVIRPDNTYEV 36
DB 130 FRGKKVLGDYDIKVEQAEFSEL-NLVAHADGTYAV 163

RESULT 13
US-09-129-668-3
Sequence 3, Application US/09129668B
Patent No. 6429010
GENERAL INFORMATION:
APPLICANT: Greengard, Paul
APPLICANT: Porton, Barbara
APPLICANT: Kao, Hung-Teh
TITLE OF INVENTION: DNA ENCODING THE HUMAN SYNAPSIN III GENE AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 600-1-202 CIP
CURRENT APPLICATION NUMBER: US/09/129,668B
CURRENT FILING DATE: 1998-08-05
EARLIER APPLICATION NUMBER: 08/906,865
EARLIER FILING DATE: 1997-08-06
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 3
LENGTH: 582
TYPE: PRT
ORGANISM: Homo sapiens
US-09-129-668-3

Query Match 23.8%; Score 61.5; DB 4; Length 582;
Best Local Similarity 40.0%; Pred. No. 1.9;
Matches 14; Conservative 7; Mismatches 13; Indels 1; Gaps 1;

QY 2 YGKQNVLINKDIRCKDDETHLYTLVIRPDNTYEV 36
DB 130 FRGKKVLGDYDIKVEQAEFSEL-NLVAHADGTYAV 163

RESULT 14
US-09-252-991A-18861
Sequence 18861, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 18861
LENGTH: 588
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18861

Query Match 21.3%; Score 55; DB 4; Length 588;
Best Local Similarity 48.0%; Pred. No. 17;
Matches 12; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

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Job time : 10.9529 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 4, 2004, 13:06:03 ; Search time 36.0294 Seconds
(without alignments)
437.647 Million cell updates/sec

Title: US-09-807-148-6

Perfect score: 258

Sequence: 1 NYKGNVLINKIRCKDEF.....PDNTYEVKIDNSQVSGSLE 49

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Gapop 10.0 , Gapext 0.5

Searched: 1351062 seqs, 321799191 residues

Total number of hits satisfying chosen parameters: 1351062

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
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7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
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12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
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18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	258	100.0	61	10	US-09-828-000-8
2	258	100.0	61	15	Sequence 8, Appli
3	258	100.0	180	10	US-09-828-000-3
4	258	100.0	180	15	Sequence 3, Appli
5	258	100.0	416	10	US-09-828-000-2
6	258	100.0	416	14	US-10-316-253-2
7	258	100.0	416	14	US-10-316-253-4
8	258	100.0	416	14	US-10-316-253-6
9	258	100.0	416	15	US-10-405-588-2
10	258	100.0	417	10	US-09-906-392A-36
11	258	100.0	417	14	US-10-161-359-29
12	258	100.0	417	15	US-10-367-093-14
13	179	69.4	395	15	US-10-369-493-6343
14	175	67.8	35	10	US-09-828-000-7
15	175	67.8	35	15	US-10-405-588-7

Sequence 4, Appli
Sequence 4, Appli
Sequence 32394, A
Sequence 55877, A
Sequence 38848, A
Sequence 48930, A
Sequence 46544, A
Sequence 70304, A
Sequence 114914, A
Sequence 114860, A
Sequence 46405, A
Sequence 69619, A
Sequence 46859, A
Sequence 46, Appli
Sequence 2, Appli
Sequence 122222, A
Sequence 44768, A
Sequence 277445, A
Sequence 45264, A
Sequence 70140, A
Sequence 65495, A
Sequence 153809, A
Sequence 44621, A
Sequence 54957, A
Sequence 153808, A
Sequence 190956, A
Sequence 46228, A
Sequence 55955, A
Sequence 190958, A
Sequence 57598, A

US-09-828-000-4
US-10-405-588-4
US-10-029-386-32394
US-10-767-701-55877
US-10-425-114-38848
US-10-425-114-48930
US-10-767-701-46544
US-10-425-114-70304
US-10-437-963-114914
US-10-437-963-114860
US-10-425-114-46405
US-10-425-114-69619
US-10-425-114-46859
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US-10-437-963-122222
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US-10-767-701-45264
US-10-425-114-70140
US-10-425-114-65495
US-10-424-599-153809
US-10-425-114-44621
US-10-425-114-54957
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US-10-424-599-190956
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US-10-424-599-190958
US-10-425-114-57598

ALIGNMENTS

RESULT 1

US-09-828-000-8
; Sequence 8, Application US/09828000
; Publication No. US20030078198A1
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/09/828,000
; CURRENT FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 8
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Fragment 5
US-09-828-000-8

Query Match 100.0%; Score 258; DB 10; Length 61;
Best Local Similarity 100.0%; Pred. No. 2.3e-27;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYKGNVLINKIRCKDEFTHLYTLVIRPDNTYEVKIDNSQVSGSLE 49
DB 13 NYKGNVLINKIRCKDEFTHLYTLVIRPDNTYEVKIDNSQVSGSLE 61

RESULT 2

US-10-405-588-8
; Sequence 8, Application US/10405588
; Publication No. US20030216299A1
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/10/405,588
; CURRENT FILING DATE: 2003-04-01
; PRIOR APPLICATION NUMBER: US/09/828,000

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; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Fragment 5
US-10-405-588-8

Query Match      100.0%; Score 258; DB 15; Length 61;
Best Local Similarity 100.0%; Pred. No. 2.3e-27;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYKGNVLINKDIRCKDDEFTHTLTVLRPDNTYEVKIDNSQVESGSLE 49
Db 13 NYKGNVLINKDIRCKDDEFTHTLTVLRPDNTYEVKIDNSQVESGSLE 61

RESULT 3
US-09-828-000-3
; Sequence 3, Application US/09828000
; Publication No. US20030078198A1
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/09/828,000
; CURRENT FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Vasostatin
US-09-828-000-3

Query Match      100.0%; Score 258; DB 10; Length 180;
Best Local Similarity 100.0%; Pred. No. 8.9e-27;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYKGNVLINKDIRCKDDEFTHTLTVLRPDNTYEVKIDNSQVESGSLE 49
Db 132 NYKGNVLINKDIRCKDDEFTHTLTVLRPDNTYEVKIDNSQVESGSLE 180

RESULT 4
US-10-405-588-3
; Sequence 3, Application US/10405588
; Publication No. US20030216299A1
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/10/405,588
; CURRENT FILING DATE: 2003-04-01
; PRIOR APPLICATION NUMBER: US/09/828,000
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Vasostatin
US-10-405-588-3

Query Match      100.0%; Score 258; DB 15; Length 180;
Best Local Similarity 100.0%; Pred. No. 8.9e-27;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Fragment 5
US-10-405-588-8

Query Match      100.0%; Score 258; DB 15; Length 61;
Best Local Similarity 100.0%; Pred. No. 2.3e-27;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYKGNVLINKDIRCKDDEFTHTLTVLRPDNTYEVKIDNSQVESGSLE 49
Db 13 NYKGNVLINKDIRCKDDEFTHTLTVLRPDNTYEVKIDNSQVESGSLE 61

RESULT 5
US-09-828-000-2
; Sequence 2, Application US/09828000
; Publication No. US20030078198A1
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/09/828,000
; CURRENT FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Calreticulin
US-09-828-000-2

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Best Local Similarity 100.0%; Pred. No. 2.5e-26;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYKGNVLINKDIRCKDDEFTHTLTVLRPDNTYEVKIDNSQVESGSLE 49
Db 149 NYKGNVLINKDIRCKDDEFTHTLTVLRPDNTYEVKIDNSQVESGSLE 197

RESULT 6
US-10-316-253-2
; Sequence 2, Application US/10316253
; Publication No. US20030162706A1
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Peters, Kevin
; APPLICANT: Thompson, Larry
; APPLICANT: Wang, Feng
; APPLICANT: Greis, Kenneth
; TITLE OF INVENTION: Angiogenesis Modulating Proteins
; FILE REFERENCE: 8865M
; CURRENT APPLICATION NUMBER: US/10/316,253
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: US 60/355,295
; PRIOR FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-316-253-2

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Best Local Similarity 100.0%; Pred. No. 2.5e-26;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NYKGNVLINKDIRCKDDEFTHTLTVLRPDNTYEVKIDNSQVESGSLE 49
Db 149 NYKGNVLINKDIRCKDDEFTHTLTVLRPDNTYEVKIDNSQVESGSLE 197

RESULT 7
US-10-316-253-4
; Sequence 4, Application US/10316253
; Publication No. US20030162706A1
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Peters, Kevin
; APPLICANT: Thompson, Larry
; APPLICANT: Wang, Feng
; APPLICANT: Greis, Kenneth
; TITLE OF INVENTION: Angiogenesis Modulating Proteins
; FILE REFERENCE: 8865M
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Query Match          100.0%; Score 258; DB 15; Length 416;
Best Local Similarity 100.0%; Pred. No. 2.5e-26;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB      149 NYKGKVLINKIRCKDDETHLYTLIVRPDNTYEYVKIDNSQVESGSUE 197

RESULT 10
US-09-906-393A-36
; Sequence 36, Application US/09906393A
; Publication No. US2003003970A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Zhou
; APPLICANT: Xiao, Wuhan
; TITLE OF INVENTION: METHOD OF PROGNOSING CANCER AND THE PROTEINS INVOLVED
; FILE REFERENCE: 1720-1-001CIP
; CURRENT APPLICATION NUMBER: US/09/906,393A
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/218,761
; PRIOR FILING DATE: 2000-07-17
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-906-393A-36

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Best Local Similarity 100.0%; Pred. No. 2.5e-26;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 NYKGKVLINKIRCKDDETHLYTLIVRPDNTYEYVKIDNSQVESGSLE 49
DB      149 NYKGKVLINKIRCKDDETHLYTLIVRPDNTYEYVKIDNSQVESGSLE 197

RESULT 11
US-10-161-959-29
; Sequence 29, Application US/10161959
; Publication No. US20030096748A1
; GENERAL INFORMATION:
; APPLICANT: Holoshitz, Joseph
; APPLICANT: Ling, Song
; TITLE OF INVENTION: Methods and Compositions for the Treatment of Diseases
; TITLE OF INVENTION: Signal Transduction Aberrations
; FILE REFERENCE: UM-07135
; CURRENT APPLICATION NUMBER: US/10/161,959
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: 60/295,691
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-161-959-29

Query Match          100.0%; Score 258; DB 14; Length 417;
Best Local Similarity 100.0%; Pred. No. 2.5e-26;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 NYKGKVLINKIRCKDDETHLYTLIVRPDNTYEYVKIDNSQVESGSLE 49
DB      149 NYKGKVLINKIRCKDDETHLYTLIVRPDNTYEYVKIDNSQVESGSLE 197

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RESULT 12
US-10-367-093-14
; Sequence 14, Application US/10367093
; Publication No. US20030216315A1
; GENERAL INFORMATION:
; APPLICANT: Duke University
; APPLICANT: Nicchitta, Chris
; APPLICANT: Baker-LePain, Julie
; TITLE OF INVENTION: MODULATION OF IMMUNE RESPONSE BY NON-PEPTIDE BINDING STRESS RESPON
; FILE REFERENCE: 180/145
; CURRENT APPLICATION NUMBER: US/10/367,093
; CURRENT FILING DATE: 2003-02-13
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-367-093-14

Query Match          100.0%; Score 258; DB 15; Length 417;
Best Local Similarity 100.0%; Pred. No. 2.5e-26;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYKGNVLINKDIRCKDDFTHTLYTLIVRPDNTYEVKIDNSQVSGSLE 49
Db 149 NYKGNVLINKDIRCKDDFTHTLYTLIVRPDNTYEVKIDNSQVSGSLE 197

RESULT 13
US-10-369-493-6343
; Sequence 6343, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 6343
; LENGTH: 395
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-6343

Query Match          69.4%; Score 179; DB 15; Length 395;
Best Local Similarity 67.3%; Pred. No. 1.2e-15;
Matches 33; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 NYKGNVLINKDIRCKDDFTHTLYTLIVRPDNTYEVKIDNSQVSGSLE 49
Db 144 NYKGNVLINKDIRCKDDFTHTLYTLIVRPDNTYEVKIDNSQVSGSLE 192

RESULT 14
US-09-828-000-7
; Sequence 7, Application US/09828000
; Publication No. US20030078198A1
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasoestatins as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/09/828,000
; CURRENT FILING DATE: 2001-04-06
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; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Fragment 4
US-09-828-000-7

Query Match          67.8%; Score 175; DB 10; Length 35;
Best Local Similarity 100.0%; Pred. No. 2.1e-16;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYKGNVLINKDIRCKDDFTHTLYTLIVRPDN 32
Db 4 NYKGNVLINKDIRCKDDFTHTLYTLIVRPDN 35

RESULT 15
US-10-405-588-7
; Sequence 7, Application US/10405588
; Publication No. US20030216299A1
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasoestatins as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/10/405,588
; CURRENT FILING DATE: 2003-04-01
; PRIOR APPLICATION NUMBER: US/09/828,000
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Fragment 4
US-10-405-588-7

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Best Local Similarity 100.0%; Pred. No. 2.1e-16;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 4 NYKGNVLINKDIRCKDDFTHTLYTLIVRPDN 35

Search completed: October 4, 2004, 13:17:33
Job time : 36.0294 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 4, 2004, 12:52:12 ; Search time 7.20588 Seconds
(without alignments)
354.077 Million cell updates/sec

Title: US-09-807-148-6

Perfect score: 258
Sequence: 1 NYKGNVLINKIRCKDEF.....PDNTYEVKIDNSQVESGSL 49

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	258	100.0	416	1	CRTC_MOUSE
2	258	100.0	416	1	CRTC_RAT
3	258	100.0	417	1	CRTC_CRIGR
4	258	100.0	417	1	CRTC_HUMAN
5	258	100.0	418	1	CRTC_RABIT
6	253	98.1	417	1	CRT1_BOVIN
7	253	98.1	421	1	CRT2_BOVIN
8	209	81.0	406	1	CRTC_DROME
9	182	70.5	388	1	RALI_ONCVO
10	182	70.5	393	1	CRTC_SCHMA
11	179	69.4	395	1	CRTC_CABEL
12	164	63.6	420	1	CRTC_CHLRE
13	148.5	57.6	424	1	CRTC_DICDI
14	147	57.0	380	1	CRTC_MOUSE
15	145	56.2	384	1	CRTC_HUMAN
16	145	56.2	421	1	CRTC_PROAR
17	144	55.8	416	1	CRTC_BETVU
18	143	55.4	415	1	CRTC_RICCO
19	143	55.4	424	1	CRTC_MAIZE
20	142	55.0	420	1	CRTC_ARATH
21	138	53.5	425	1	CRT1_ARATH
22	136	52.7	401	1	CRTC_EUGR
23	135	52.3	416	1	CRTC_NICPL
24	134	51.9	424	1	CRTC_ORYSA
25	132	51.2	424	1	CRTC_ARATH
26	128.5	49.8	416	1	CRTC_BERST
27	101	39.1	591	1	CALX_MOUSE
28	101	39.1	591	1	CALX_RAT
29	101	39.1	592	1	CALX_HUMAN
30	100	38.8	593	1	CALX_CANFA
31	95	36.8	610	1	CALG_HUMAN
32	93.5	36.2	611	1	CALG_MOUSE
33	89	34.5	560	1	CALX_SCHPO

34 78 30.2 619 1 CALX_CABEL
35 71 27.5 546 1 CALX_SOYBN
36 68 26.4 530 1 CALX_ARATH
37 68 26.4 540 1 CALX_HELTU
38 64 24.8 540 1 MTAL_ACICA
39 62 24.0 532 1 CAX2_ARATH
40 61.5 23.8 582 1 SYN2_HUMAN
41 60.5 23.4 586 1 SYN2_RAT
42 60 23.3 474 1 LAM3_MOUSE
43 60 23.3 592 1 LAM2_MOUSE
44 58 22.5 763 1 CADQ_MOUSE
45 57 22.1 362 1 YCIS_YEAST

P34652 caenorhabdi
Q39817 glycine max
P29402 arabidopsis
Q39994 helianthus
P25201 acinetobact
Q38798 arabidopsis
Q92777 homo sapien
O63537 rattus norv
P48680 mus musculu
P21619 mus musculu
P59862 mus musculu
P25366 saccharomyc

ALIGNMENTS

RESULT 1
CRTC_MOUSE
ID CRTC_MOUSE STANDARD; PRT; 416 AA.
AC P14211;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Calreticulin precursor (CRP55) (Calregulin) (HACBP) (ERP60).
GN CALR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 18-48 AND 129-161.
RX STRAIN=BAIB/C; TISSUE=Liver;
RC MEDLINE=90059955; PubMed=2583110;
RA Smith M.J., Koch G.L.E.;
RT "Multiple zones in the sequence of calreticulin (CRP55, calregulin, HACBP), a major calcium binding ER/SR protein.";
RL EMBO J. 8:3581-3586 (1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93013037; PubMed=1398135;
RA Mazzarella R.A., Gold P., Cunningham M., Green M.;
RT "Determination of the sequence of an expressible cDNA clone encoding ERp60/calregulin by the use of a novel nested set method.";
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=FVB/N-3; TISSUE=Mammary gland;
MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Brownstein M.J., Udutin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunatane P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Hellon E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakeley R.C., Touchman J.W., Green E.D., Dickinson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywicki M.J., Skalska U., Smallos D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [4]
RP SEQUENCE OF 18-38;
RT TISSUE=Fibroblast;
RC MEDLINE=95009907; PubMed=7523108;
RX

RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
 RT "Separation and sequencing of familial and novel murine proteins
 RL using preparative two-dimensional gel electrophoresis.",
 CC Electrophoresis 15:735-745(1994).
 CC -1- FUNCTION: This protein binds calcium. There are both high and
 CC low affinity calcium-binding sites.
 CC -1- SUBUNIT: Monomer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
 CC -1- SIMILARITY: Belongs to the calreticulin family.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL; X14926; CAA33053.1; -
 DR EMBL; M22988; AAA37569.1; -
 DR EMBL; BC003453; AAH03453.1; -
 DR PIR; S06763; S06763.
 DR SWISS-2DPAGE; P14211; MOUSE.
 DR MGD; MGI:88252; Calr.
 DR GO; GO:0005509; F:calcium ion binding; IDA.
 DR InterPro; IPR009033; Calret_calmex_P.
 DR InterPro; IPR001580; Calreticulin.
 DR InterPro; IPR008985; ConA-like lec_gl.
 DR Pfam; PF00262; calreticulin; 1.
 DR PRINTS; PIRSF002356; Calreticulin; 1.
 DR PROSITE; PS00626; CALRETICULIN.
 DR PROSITE; PS001866; Calreticulin; 1.
 DR PROSITE; PS00014; ER_TARGET; 1.
 DR PROSITE; PS00803; CALRETICULIN_1; 1.
 DR PROSITE; PS00804; CALRETICULIN_2; 1.
 DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
 FT SIGNAL 1 17
 FT CHAIN 18 416
 FT DOMAIN 18 197
 FT DOMAIN 198 308
 FT DOMAIN 309 416
 FT DOMAIN 191 255
 FT REPEAT 191 202
 FT REPEAT 210 221
 FT REPEAT 227 238
 FT REPEAT 244 255
 FT DOMAIN 259 297
 FT REPEAT 259 269
 FT REPEAT 273 283
 FT REPEAT 287 297
 FT DOMAIN 351 407
 FT DISULFID 137 163
 FT SITE 413 416
 FT SEQUENCE 416 AA; 47994 MW; 24C03B00913408D8 CRC64;
 Query Match 100.0%; Score 258; DB 1; Length 416;
 Best Local Similarity 100.0%; Pred. No. 8.1e-26;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NYKGNVLINKDIRCKDEFFHLTVLPNTYEVKIDNSQVSGSLE 49
 DB 149 NYKGNVLINKDIRCKDEFFHLTVLPNTYEVKIDNSQVSGSLE 197
 RESULT 2
 CRTC_RAT STANDARD; PRT; 416 AA.
 AC F18418; P10452;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Calreticulin precursor (CRP55) (Calregulin) (HACBP) (Erp60) (CALBP)
 DE (Calcium-binding protein 3) (CABP3).
 GN CALR.
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CC NCBI_taxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Brain cortex;
 RX MEDLINE=90370496; PubMed=2395661;
 RA Murthy K.K., Banville D., Srikanth C.B., Carrier F., Bell A.,
 RA Holmes C., Patel Y.C.;
 RT "Structural homology between the rat calreticulin gene product and
 RT the Onchocerca volvulus antigen Ral-1.";
 RL Nucleic Acids Res. 18:4933-4933(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RX MEDLINE=93202172; PubMed=8453984;
 RA Nakamura M., Moriya M., Baba T., Michikawa Y., Yamanobe T., Arai K.,
 RA Okinaga S., Kobayashi T.;
 RT "An endoplasmic reticulum protein, calreticulin, is transported into
 RT the acrosome of rat sperm.";
 RL Exp. Cell Res. 205:101-110(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Liver;
 RX MEDLINE=95181573; PubMed=7876339;
 RA Soennichsen B., Fuelektrug J., van Nguyen P., Diekmann W.,
 RA Robinson D.G., Mieskes G.;
 RT "Retention and retrieval: both mechanisms cooperate to maintain
 RT calreticulin in the endoplasmic reticulum.";
 RL J. Cell Sci. 107:2705-2717(1994).
 RN [4]
 RP SEQUENCE OF 270-358 FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RX Lone Y.C., Bailly A., Latruffe N.;
 RL Submitted (DEC-1988) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 18-29.
 RX MEDLINE=91054414; PubMed=2241926;
 RA Treves S., de Mattei M., Lanfredi M., Villa A., Green N.M.,
 RA MacLennan D.H., Meldolesi J., Pozzan T.;
 RT "Calreticulin is a candidate for a calsequestrin-like function in
 RT Ca2(+)-storage compartments (calciosomes) of liver and brain.";
 RL Biochem. J. 271:473-480(1990).
 RN [6]
 RP SEQUENCE OF 18-32.
 RC STRAIN=Sprague-Dawley; TISSUE=Testis;
 RX MEDLINE=92360010; PubMed=1497855;
 RA Nakamura M., Michikawa Y., Baba T., Okinaga S., Arai K.;
 RT "Calreticulin is present in the acrosome of spermatids of rat
 RT testis.";
 RL Biochem. Biophys. Res. Commun. 186:668-673(1992).
 RN [7]
 RP SEQUENCE OF 18-32.
 RC STRAIN=LEC; TISSUE=Liver;
 RX MEDLINE=94072621; PubMed=8251535;
 RA Yokoi T., Nagayama S., Kajiwara R., Kawaguchi Y., Horiuchi R.,
 RA Kamataki T.;
 RT "Identification of protein disulfide isomerase and calreticulin as
 RT autoimmunity antigens in LEC strain of rats.";
 RL Biochim. Biophys. Acta 1158:339-344(1993).
 CC -1- FUNCTION: This protein binds calcium. There are both high and low
 CC affinity calcium-binding sites.
 CC -1- SUBUNIT: Monomer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
 CC -1- SIMILARITY: Belongs to the calreticulin family.
 CC -1- CAUTION: Was originally (Ref.2) thought to be D-beta-
 CC hydroxybutyrate dehydrogenase.
 CC
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CC EMBL; D78308; BA01345.1; -
 CC EMBL; X53363; CAA37446.1; -
 CC EMBL; X13702; CAA31987.1; ALT_SEQ.
 CC EMBL; X79327; CAA55890.1; -
 CC FIR; JH0819; JH0819.
 CC PDB; 1LHN; 26-FEB-02.
 CC PDB; 1K91; 12-OCT-02.
 CC PDB; 1K9C; 12-OCT-02.

DR InterPro; IPR009033; Calret calnex P.
 DR InterPro; IPR001580; Calreticulin.
 DR InterPro; IPR008985; ConA like lec gl.
 DR InterPro; IPR000886; ER target_S.
 DR Pfam; PF00262; calreticulin; 1.
 DR PIRSF; PIRSF002356; Calreticulin; 1.
 DR PRINTS; PR00626; Calreticulin.
 DR ProDom; PD001866; Calreticulin; 1.
 DR PROSITE; PS00104; ER TARGET; 1.
 DR PROSITE; PS00803; CALRETICULIN 1; 1.
 DR PROSITE; PS00804; CALRETICULIN 2; 1.
 DR PROSITE; PS00805; CALRETICULIN REPEAT; 3.
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal; 3D-structure.

FT SIGNAL 1 17
 FT CHAIN 18 416 CALRETICULIN.
 FT DOMAIN 18 197 N-DOMAIN.
 FT DOMAIN 198 308 P-DOMAIN.
 FT DOMAIN 309 416 C-DOMAIN.
 FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.
 FT REPEAT 191 202 1-1.
 FT REPEAT 210 221 1-2.
 FT REPEAT 227 238 1-3.
 FT REPEAT 244 255 1-4.
 FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.
 FT REPEAT 273 283 2-1.
 FT REPEAT 287 297 2-2.
 FT REPEAT 351 407 ASP/GLU/LYS-RICH.
 FT DOMAIN 137 163 BY SIMILARITY.
 FT DISULFID 137 163
 FT SITE 413 416 PREVENT SECRETION FROM ER.
 FT SITE 416 416 PREVENT SECRETION FROM ER.
 SQ SEQUENCE 416 AA; 47995 MW; 26713CEDJ1A2970 CRC64;

Query Match 100.0%; Score 258; DB 1; Length 416;
 Best Local Similarity 100.0%; Pred. No. 8.1e-26;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYKGNVLINKDIRCKDDEFTLYTLVPRDNTYEVKIDNSQVSGSLE 49
 DB 149 NYKGNVLINKDIRCKDDEFTLYTLVPRDNTYEVKIDNSQVSGSLE 197

RESULT 3

ID CRIC CRIGR STANDARD; PRT; 417 AA.
 AC O8K3H7;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Calreticulin precursor (CRP55) (Calregulin) (HACBP) (ERP60).
 GN CALR.
 OS Cricetulus griseus (Chinese hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Cricetulus.
 OX NCBI_TaxID=10029;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Chung J.Y., Lee G.M.;

RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: This protein binds calcium. There are both high and low
 CC affinity calcium-binding sites.
 CC -!- SUBUNIT: Monomer.
 CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
 CC -!- SIMILARITY: Belongs to the calreticulin family.

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 CC or send an email to license@isb-sib.ch).

CC EMBL; AY100688; AAM48568.1; -
 DR InterPro; IPR009033; Calret calnex P.
 DR InterPro; IPR001580; Calreticulin.
 DR InterPro; IPR008985; ConA like lec gl.
 DR InterPro; IPR000886; ER target_S.
 DR Pfam; PF00262; calreticulin; 1.
 DR PIRSF; PIRSF002356; Calreticulin; 1.
 DR PRINTS; PR00626; Calreticulin.
 DR ProDom; PD001866; Calreticulin; 1.
 DR PROSITE; PS00803; CALRETICULIN 1; 1.
 DR PROSITE; PS00804; CALRETICULIN 2; 1.
 DR PROSITE; PS00805; CALRETICULIN REPEAT; 3.
 DR PROSITE; PS00104; ER TARGET; 1.
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Glycoprotein; Signal.

FT SIGNAL 1 17 BY SIMILARITY.
 FT CHAIN 18 417 CALRETICULIN.
 FT DOMAIN 18 197 N-DOMAIN.
 FT DOMAIN 198 308 P-DOMAIN.
 FT DOMAIN 309 417 C-DOMAIN.
 FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.
 FT REPEAT 191 202 1-1.
 FT REPEAT 210 221 1-2.
 FT REPEAT 227 238 1-3.
 FT REPEAT 244 255 1-4.
 FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.
 FT REPEAT 273 283 2-1.
 FT REPEAT 287 297 2-2.
 FT REPEAT 351 407 ASP/GLU/LYS-RICH.
 FT DOMAIN 137 163 BY SIMILARITY.
 FT DISULFID 137 163
 FT SITE 414 417 PREVENT SECRETION FROM ER (POTENTIAL).
 FT SITE 417 417 PREVENT SECRETION FROM ER (POTENTIAL).
 SQ SEQUENCE 417 AA; 48242 MW; D617DA37D14F2D45 CRC64;

Query Match 100.0%; Score 258; DB 1; Length 417;
 Best Local Similarity 100.0%; Pred. No. 8.2e-26;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NYKGNVLINKDIRCKDDEFTLYTLVPRDNTYEVKIDNSQVSGSLE 49
 DB 149 NYKGNVLINKDIRCKDDEFTLYTLVPRDNTYEVKIDNSQVSGSLE 197

RESULT 4

ID CRIC HUMAN STANDARD; PRT; 417 AA.
 AC P27797;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Calreticulin precursor (CRP55) (Calregulin) (HACBP) (ERP60).
 GN CALR OR CRIC
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92013129; PubMed=1919005;


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FT DOMAIN 18 197 N-DOMAIN.
FT DOMAIN 198 308 P-DOMAIN.
FT DOMAIN 309 417 C-DOMAIN.
FT DOMAIN 255 4 X APPROXIMATE REPEATS.
FT REPEAT 191 202 1-1.
FT REPEAT 210 221 1-2.
FT REPEAT 227 238 1-3.
FT REPEAT 244 255 1-4.
FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.
FT REPEAT 259 269 2-1.
FT REPEAT 273 283 2-2.
FT REPEAT 287 297 2-3.
FT DOMAIN 351 408 ASP/GLU/LYS-RICH.
FT DISULFID 137 163 BY SIMILARITY.
FT SITE 414 17 PREVENT SECRETION FROM ER.
FT CONFLICT 35 35 MISSING (IN REF. 3).
SQ SEQUENCE 417 AA; 48141 MW; BC37C3C0F1054FB2 CRC64;

Query Match 100.0%; Score 258; DB 1; Length 417;
Best Local Similarity 100.0%; Pred. No. 8.2e-26; Indels 0; Gaps 0;
Matches 49; Conservative 0; Mismatches 0;

QY 1 NYKGNVLINKDIRCKDDETHLYTLIVRPDNTYEVKIDNSQVSGSLE 49
DB 149 NYKGNVLINKDIRCKDDETHLYTLIVRPDNTYEVKIDNSQVSGSLE 197

RESULT 5
CRIC RABIT STANDARD; PRT; 418 AA.
AC P15253;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Calreticulin precursor (CRP55) (Calregulin) (HACBP) (ERP60).
GN CALR.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;

[1]
RN SEQUENCE FROM N.A.
RP TISSUE=Slow-twitch skeletal muscle;
RX MEDLINE=90094320; PubMed=2600080;
RA Fliegel L., Burns K., MacLennan D.H., Reithmeier R.A.F., Michalak M.;
RT "Molecular cloning of the high affinity calcium-binding protein
(calsequestrin) of skeletal muscle sarcoplasmic reticulum.";
RL J. Biol. Chem. 264:21522-21528(1989).

[2]
RN SEQUENCE FROM N.A.
RP TISSUE=Fast-twitch skeletal muscle;
RX MEDLINE=91282795; PubMed=2059224;
RA Fliegel L., Michalak M.;
RT "Fast-twitch and slow-twitch skeletal muscles express the same
isoform of calreticulin.";
RL Biochem. Biophys. Res. Commun. 177:979-984(1991).

[3]
RN SEQUENCE OF 18-36.
RX MEDLINE=91054414; PubMed=2241326;
RA Treves S., de Mattei M., Ianfredi M., Villa A., Green N.M.,
RA MacLennan D.H., Meldolesi J., Pozzan T.;
RT "Calreticulin is a candidate for a calsequestrin-like function in
Ca2(+)-storage compartments (calciosomes) of liver and brain.";
RL Biochem. J. 271:473-480(1990).

[4]
RN SEQUENCE OF 18-46.
RX MEDLINE=92013375; PubMed=2016321;
RA Milner R.E., Baken S., Shemanko C., Carpenter M.R., Smillie L.,
RA Vance J.E., Opas M., Michalak M.;
RT "Calreticulin, and not calsequestrin, is the major calcium binding
protein of smooth muscle sarcoplasmic reticulum and liver endoplasmic
reticulum.";
RL J. Biol. Chem. 266:7155-7165(1991).

```

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[5]
RN PARTIAL SEQUENCE.
RP TISSUE=Lung;
RX MEDLINE=92002038; PubMed=1911780;
RA Guan S., Fallick A.M., Williams D.E., Cashman J.R.;
RT "Evidence for complex formation between rabbit lung flavin-containing
monooxygenase and calreticulin.";
RL Biochemistry 30:9892-9900(1991).
CC -!- FUNCTION: This protein binds calcium. There are both high and low
affinity calcium-binding sites.
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -!- SIMILARITY: Belongs to the calreticulin family.
CC
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CC
EMBL; J05138; AAA31188.1; -.
DR PIR; A34154; A34154.
DR PIR; C33208; C33208.
DR PIR; S13046; S13046.
DR InterPro; IPR009033; Calret calnex P.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR008985; ConA-like_lsc_gl.
DR Pfam; PF00262; calreticulin; 1.
DR PIRSF; PIRSF002356; Calreticulin.
DR PRINTS; P00626; Calreticulin; 1.
DR PRODOM; P0001866; Calreticulin; 1.
DR PROSITE; PS00014; ER TARGET; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
DR Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
FT SIGNAL 1 17
FT CHAIN 18 418 CALRETICULIN.
FT DOMAIN 18 197 N-DOMAIN.
FT DOMAIN 198 308 P-DOMAIN.
FT DOMAIN 309 418 4 X APPROXIMATE REPEATS.
FT DOMAIN 191 202 1-1.
FT REPEAT 191 202 1-1.
FT REPEAT 210 221 1-2.
FT REPEAT 227 238 1-3.
FT REPEAT 244 255 1-4.
FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.
FT REPEAT 259 269 2-1.
FT REPEAT 273 283 2-2.
FT REPEAT 287 297 2-3.
FT DOMAIN 351 408 ASP/GLU/LYS-RICH.
FT DISULFID 137 163 BY SIMILARITY.
FT SITE 415 418 PREVENT SECRETION FROM ER.
FT VARIANT 35 35 E -> D. (IN REF. 5).
FT CONFLICT 90 90 P -> T. (IN REF. 5).
SQ SEQUENCE 418 AA; 48275 MW; B6082B689DC763A6 CRC64;

Query Match 100.0%; Score 258; DB 1; Length 418;
Best Local Similarity 100.0%; Pred. No. 8.2e-26;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYKGNVLINKDIRCKDDETHLYTLIVRPDNTYEVKIDNSQVSGSLE 49
DB 149 NYKGNVLINKDIRCKDDETHLYTLIVRPDNTYEVKIDNSQVSGSLE 197

RESULT 6
CRIC BOVIN STANDARD; PRT; 417 AA.
ID CRT1_BOVIN
AC P52193; Q8SQ53;

```

DT 01-OCT-1996 (Rel. 34, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Calreticulin, brain isoform 1 precursor (CRP55) (Calregulin) (HACBP).
 GN CALR OR CRT.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Hossain M.A., Takuwa K., Minakata H., Nakajima T.;
 RT "Bovine brain calreticulin."
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 18-417.
 RC TISSUE=Brain;
 RA MEDLINE=94183174; PubMed=8135753;
 RT Matsuo K., Seta K., Yamakawa Y., Okuyama T., Shinoda T., Isobe T.;
 RL "Covalent structure of bovine brain calreticulin."
 RL Biochem. J. 298:435-442(1994).
 CC -!- FUNCTION: This protein binds calcium. There are both high and low
 CC affinity calcium-binding sites.
 CC -!- SUBUNIT: Monomer.
 CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
 CC -!- SIMILARITY: Belongs to the calreticulin family.
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 CC
 CC EMBL; AB067687; BAB86913.1;
 DR InterPro; IPR009033; Calret_calmex_P.
 DR InterPro; IPR001580; Calreticulin.
 DR InterPro; IPR008985; ConA_like_lect_g1.
 DR Pfam; PF00262; Calreticulin; 1.
 DR Pfam; PF00262; Calreticulin; 1.
 DR PRINTS; PIRSF002356; Calreticulin; 1.
 DR PROSITE; PS00626; CALRETICULIN.
 DR PROSITE; PS00014; ER_TARGET; 1.
 DR PROSITE; PS00803; CALRETICULIN 1; 1.
 DR PROSITE; PS00804; CALRETICULIN 2; 1.
 DR PROSITE; PS00805; CALRETICULIN REPEAT; 3.
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Glycoprotein; Signal.
 FT SIGNAL 1 17
 FT CHAIN 18 417 CALRETICULIN, BRAIN ISOFORM 1.
 FT DOMAIN 18 197 N-DOMAIN.
 FT DOMAIN 198 308 P-DOMAIN.
 FT DOMAIN 309 417 C-DOMAIN.
 FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.
 FT REPEAT 191 202 1-1.
 FT REPEAT 202 221 1-2.
 FT REPEAT 227 238 1-3.
 FT REPEAT 244 255 1-4.
 FT REPEAT 259 297 3 X APPROXIMATE REPEATS.
 FT REPEAT 259 269 2-1.
 FT REPEAT 273 283 2-2.
 FT REPEAT 287 297 2-3.
 FT REPEAT 351 407 ASP/GLU/LYS-RICH.
 FT DOMAIN 137 163 N-LINKED (GLCNAC...)
 FT CARBOHYD 179 179 PRESENT SECRETION FROM ER (POTENTIAL).
 FT SITE 414 417
 FT SEQUENCE 417 AA; 48038 MW; 7BF812C7B5417B59 CRC64;
 SQ
 Query Match 98.1%; Score 253; DB 1; Length 417;
 Best Local Similarity 98.0%; Pred. No. 3.6e-25;

Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NYKGNVLINIKDKDETHLYTLVRPDNTYEVKIDNSQVSGSLE 49
 DB 149 NYKGNVLINIKDKDETHLYTLVRPDNTYEVKIDNSQVSGSLE 197
 RESULT 7
 CRT2_BOVIN STANDARD; PRT; 421 AA.
 ID P42918;
 AC 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Calreticulin, brain isoform 2 precursor (CRP55) (Calregulin) (HACBP).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA MEDLINE=93385184; PubMed=8373827;
 RX Liu N., Fine R.B., Johnson R.J.;
 RL "Comparison of cDNAs from bovine brain coding for two isoforms of
 RL calreticulin."
 RL Biochim. Biophys. Acta 1202:70-76(1993).
 CC -!- FUNCTION: This protein binds calcium. There are both high and low
 CC affinity calcium-binding sites.
 CC -!- SUBUNIT: Monomer (by similarity).
 CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
 CC -!- SIMILARITY: Belongs to the calreticulin family.
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 CC
 CC EMBL; L13462; AAC37307.1;
 DR PIR; S36799; S36799.
 DR InterPro; IPR009033; Calret_calmex_P.
 DR InterPro; IPR001580; Calreticulin.
 DR InterPro; IPR008985; ConA_like_lect_g1.
 DR InterPro; IPR008986; ER_target_S.
 DR Pfam; PF00262; Calreticulin; 1.
 DR Pfam; PF00262; Calreticulin; 1.
 DR PRINTS; PIRSF002356; Calreticulin; 1.
 DR PROSITE; PS00626; CALRETICULIN.
 DR PROSITE; PS00014; ER_TARGET; 1.
 DR PROSITE; PS00803; CALRETICULIN 1; 1.
 DR PROSITE; PS00804; CALRETICULIN 2; 1.
 DR PROSITE; PS00805; CALRETICULIN REPEAT; 3.
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
 FT SIGNAL 1 34
 FT CHAIN 35 421 CALRETICULIN, BRAIN ISOFORM 2.
 FT DOMAIN 35 201 N-DOMAIN.
 FT DOMAIN 202 312 P-DOMAIN.
 FT DOMAIN 313 421 C-DOMAIN.
 FT DOMAIN 195 259 4 X APPROXIMATE REPEATS.
 FT REPEAT 195 206 1-1.
 FT REPEAT 214 225 1-2.
 FT REPEAT 231 242 1-3.
 FT REPEAT 248 259 1-4.
 FT DOMAIN 263 301 3 X APPROXIMATE REPEATS.
 FT REPEAT 263 273 2-1.
 FT REPEAT 277 287 2-2.
 FT REPEAT 291 301 2-3.
 FT DOMAIN 366 411 ASP/GLU/LYS-RICH.
 FT DISULFID 141 167 BY SIMILARITY.

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FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SITE 418 421 PREVENT SECRETION FROM ER.
SQ SEQUENCE 421 AA; 48812 MW; 0257E959F71528BC CRC64;

Query Match
Best Local Similarity 98.1%; Score 253; DB 1; Length 421;
Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NYKGNVLINKDRCKDETHLYTLVRPNTYEVKIDNSQVSGSLE 49
DB 153 NYKGNVLINKDRCKDETHLYTLVRPNTYEVKIDNSQVSGSLE 201

RESULT 8
CRIC DROME STANDARD; PRT; 406 AA.
AC P29413; Q9VHA3;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Calreticulin precursor (CRP55) (Calregulin) (HACBP).
GN CRC OR CG9429.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN RN SEQUENCE FROM N.A.
RP MEDLINE=93208374; PubMed=1296819;
RX Smith M.J.;
RA "Nucleotide sequence of a Drosophila melanogaster gene encoding a
RT calreticulin homologue."
RL DNA Seq. 3:247-250(1992).
RN RN SEQUENCE FROM N.A.
RC STRAIN=Berkely;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers J.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-pfankoch C., Baldwin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Herman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Buesam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke K., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K.J., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Foeller C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Hewland T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laslo P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.F., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,

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RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
RN RN SEQUENCE OF 91-124 AND 182-220.
RP MEDLINE=90307981; PubMed=2365822;
RA McCaulliffe D.P., Zappi E., Lieu T.S., Michalak M., Sontheimer R.D.,
RA Capra J.D.;
RT "A human Ro/SS-A autoantigen is the homologue of calreticulin and is
RT highly homologous with oncohercal RAL-1 antigen and an aplasia
RT 'memory molecule'."
RL J. Clin. Invest. 86:332-335(1990).
CC -!- FUNCTION: This protein binds calcium. There are both high and low
CC affinity calcium-binding sites.
CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -!- SIMILARITY: Belongs to the calreticulin family.
CC
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CC
CC EMBL: Y64461; CAA45791.1; -
CC EMBL: AE003683; AAF54416.1; -
CC FIR: A56637; A56637.
CC Flybase; FBgn005585; Crc.
CC GO: GO:007417; P:central nervous system development; IMP.
CC InterPro; IPR009033; Calret calnex P.
CC InterPro; IPR001580; Calreticulin.
CC InterPro; IPR008985; Coxa like lec_gl.
CC InterPro; IPR000886; ER_target_S.
CC Pfam; PF00262; calreticulin; 1.
CC PIRSF; PIRSF002356; Calreticulin; 1.
CC PRINTS; PR00626; CALRETICULIN.
CC ProDom; PD001866; Calreticulin; 1.
CC PROSITE; PS00014; ER_TARGET; 1.
CC PROSITE; PS00803; CALRETICULIN_1; 1.
CC PROSITE; PS00804; CALRETICULIN_2; 1.
CC PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
CC Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
CC SIGNAL 1 17 POTENTIAL.
CC CHAIN 18 406 CALRETICULIN.
CC CONFLICT 107 107 G -> A (IN REF. 3).
CC CONFLICT 184 184 V -> L (IN REF. 3).
CC SEQUENCE 406 AA; 48808 MW; 65D72C69D0BEC427 CRC64;
SQ
Query Match 81.0%; Score 209; DB 1; Length 406;
Best Local Similarity 79.6%; Pred. No. 1.7e-19;
Matches 39; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
QY 1 NYKGNVLINKDRCKDETHLYTLVRPNTYEVKIDNSQVSGSLE 49
DB 149 SYKGNHLISKDRCKDVYTHYTLVRPNTYEVKIDNSQVSGSLE 197

RESULT 9
RAL1 ONCVO STANDARD; PRT; 388 AA.
ID RAL1 ONCVO
AC P11012;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE RAL-1 protein precursor (41 kDa larval antigen).
GN RAL1
OS Onchocerca volvulus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
OC Onchocercidae; Onchocerca.
OX NCBI_TaxID=6282;
RN RN SEQUENCE FROM N.A.
RP

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CRTC_CABEL
ID CRTC_CABEL STANDARD; PRT; 395 AA.
AC P27798;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Calreticulin precursor.
GN CRT-1 OR Y38A10A.5.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=92329978; PubMed=1627827;
RA Smith M.J.;
RT "A C. elegans gene encodes a protein homologous to mammalian
RL calreticulin."
RL DNA Seq. 2:235-240 (1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Bauer C., Courtney L., LaPlant Y.;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP REVISIONS.
RA Waterston R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RC -1- FUNCTION: This protein binds calcium. There are both high and low
CC affinity calcium-binding sites.
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -1- SIMILARITY: Belongs to the calreticulin family.
CC
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CC
CC EMBL; X59589; CAA42159.1; -.
CC EMBL; AF125963; AAD14746.1; -.
CC PIR; S25851; S25851.
CC WormPep; Y38A10A.5; CE21562.
CC InterPro; IPR003033; Calret calnex_P.
CC InterPro; IPR001580; Calreticulin.
CC InterPro; IPR008985; Cona-like lec_gl.
CC InterPro; IPR000886; ER_target_S.
CC Pfam; PF00262; calreticulin; 1.
CC PIRSF; PIRSF002356; Calreticulin; 1.
CC PRINTS; PR00626; CALRETICULIN.
CC ProDom; PD001866; Calreticulin; 1.
CC PROSITE; PS00014; ER_TARGET; 1.
CC PROSITE; PS00803; CALRETICULIN_1; 1.
CC PROSITE; PS00804; CALRETICULIN_2; 1.
CC PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
CC Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
KW SIGNAL
FT SIGNAL 1 15
FT CHAIN 16 395
FT DOMAIN ? 192
FT DOMAIN 193 301
FT DOMAIN 302 395
FT DOMAIN 186 250
FT REPEAT 186 197
FT REPEAT 205 216
FT REPEAT 222 233
FT REPEAT 229 250
FT REPEAT 234 292
FT DOMAIN 254 264
FT REPEAT 254 268
FT REPEAT 268 278
FT REPEAT 282 292

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FT DOMAIN 332 390 ASP/GLU/LYS-RICH.
FT DISULFID 133 158 BY SIMILARITY.
FT SITE 392 395 PREVENT SECRETION FROM ER.
SQ SEQUENCE 395 AA; 45616 MW; 35CA7D2EC1D56B03 CRC64;

Query Match 69.4%; Score 179; DB 1; Length 395;
Best Local Similarity 67.3%; Pred. No. 1.3e-15;
Matches 33; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 NYGKNVLIINKDIRCKDETHLYTLVIRPDNTYEVKIDNSQVESGSL 49
DB 144 NYGKNVLIINKDIRCKDETHLYTLVIRPDNTYEVKIDNSQVESGSL 192

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RESULT 12
CRTC_CHLRE STANDARD; PRT; 420 AA.
ID CRTC_CHLRE
AC Q9STD3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Calreticulin precursor.
OS Chlamydomonas reinhardtii.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Chlamydomonadaceae; Chlamydomonas.
OX NCBI_TaxID=3055;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=137c / CC-125;
RA Zuppin A., Kaydamov C.;
RT "Cloning and characterization of a cDNA encoding Chlamydomonas
RL reinhardtii calreticulin."
CC -1- FUNCTION: This protein binds calcium. There are both high and low
CC affinity calcium-binding sites (By similarity).
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen (By similarity).
CC -1- SIMILARITY: Belongs to the calreticulin family.
CC
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CC
CC EMBL; AJ000765; CAB54526.1; -.
CC InterPro; IPR009033; Calret calnex_P.
CC InterPro; IPR001580; Calreticulin.
CC InterPro; IPR008985; Cona-like lec_gl.
CC InterPro; IPR000886; ER_target_S.
CC Pfam; PF00262; calreticulin; 1.
CC PIRSF; PIRSF002356; Calreticulin; 1.
CC PRINTS; PR00626; CALRETICULIN.
CC ProDom; PD001866; Calreticulin; 1.
CC PROSITE; PS00014; ER_TARGET; 1.
CC PROSITE; PS00803; CALRETICULIN_1; 1.
CC PROSITE; PS00804; CALRETICULIN_2; 1.
CC PROSITE; PS00805; CALRETICULIN_REPEAT; 1.
CC Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
KW SIGNAL
FT SIGNAL 1 18
FT CHAIN 19 420
FT SITE 417 420 PREVENT SECRETION FROM ER (POTENTIAL).
FT SEQUENCE 420 AA; 47327 MW; DD3BA3AFBF61C9B CRC64;

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Query Match 63.6%; Score 164; DB 1; Length 420;
Best Local Similarity 61.7%; Pred. No. 1.2e-13;
Matches 29; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 2 YGKNVLIINKDIRCKDETHLYTLVIRPDNTYEVKIDNSQVESGSL 48
DB 153 YGKNVLIINKDIRCKDETHLYTLVIRPDNTYEVKIDNSQVESGSL 199

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RESULT 13
 CRIC DICTDI STANDARD; PRT; 424 AA.
 AC Q3858;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Calreticulin precursor.
 GN CRTA.
 OS Dictyostelium discoideum (Slime mold).
 OC Eukaryota; Mycetozoa; Dictyosteliales; Dictyostelium.
 OX NCBI_TaxID=44689;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AX3;
 RX Mueller-Tauberger A., Gerisch G.;
 RA Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 RL -1- FUNCTION: This protein binds calcium. There are both high and low
 CC affinity calcium-binding sites (By similarity).
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
 CC -1- SIMILARITY: Belongs to the calreticulin family.
 CC
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 CC
 CC EMBL: U36937; AAB8719.1;
 DR DictyBase; DDB0001623; CttA.
 DR InterPro; IPR009033; Calret_calmex_P.
 DR InterPro; IPR001580; Calreticulin.
 DR InterPro; IPR008985; ConA-like lec_gl.
 DR InterPro; IPR000886; ER_target_S.
 DR Pfam; PF00262; calreticulin; 1.
 DR PIRSF; PIRSF002356; Calreticulin; 1.
 DR PRINTS; PR00626; CALRETICULIN.
 DR ProDom; PD001866; Calreticulin; 1.
 DR ProSITE; PS00804; CALRETICULIN_2; 1.
 DR ProSITE; PS00805; CALRETICULIN_REPEAT; 1.
 DR ProSITE; PS00014; ER_TARGET; 1.
 DR Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
 KW SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 424
 FT DOMAIN 191 257
 FT REPEAT 191 202
 FT REPEAT 211 222
 FT REPEAT 227 238
 FT REPEAT 246 257
 FT REPEAT 260 298
 FT REPEAT 290 270
 FT REPEAT 274 284
 FT REPEAT 288 298
 FT DISULFID 105 137
 FT SITE 421 424 BY SIMILARITY.
 SQ SEQUENCE 424 AA; 48350 MW; BAF273694FB6FC37 CRC64;
 Query Match 57.6%; Score 148.5; DB 1; Length 424;
 Best Local Similarity 53.1%; Pred. No. 1.2e-11;
 Matches 26; Conservative 12; Mismatches 10; Indels 1; Gaps 1;
 QY 1 NYKGNVLINKDI-RCKDDETHLYTLVRPDNTYEVKIDNSQVSGSL 48
 Db 148 NYKGNVLIKKKINKVETDQLTHQYTLVSPDNTYVLDVNDKIQAGNL 196
 RESULT 14
 CRIT3 MOUSE
 ID CRT3_MOUSE
 AC Q9D9Q6;

DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Calreticulin 3 precursor (Calreticulin 2).
 GN CALR3 OR CRT2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Saito T., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RA Hayashizaki Y.;
 RA "Functional annotation of a full-length mouse cDNA collection.";
 RT Nature 409:685-690 (2001).
 RL [2]
 RN IDENTIFICATION, AND TISSUE SPECIFICITY.
 RX MEDLINE=2221577; PubMed=12384296;
 RA Parson S., Rosenquist M., Sommarin M.;
 RT "Identification of a novel calreticulin isoform (Crt2) in human and
 RT mouse.";
 RL Gene 297:151-158 (2002).
 CC -1- FUNCTION: Ca(2+)-binding chaperone (By similarity).
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen (By similarity).
 CC -1- SIMILARITY: Belongs to the calreticulin family.
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 CC
 CC EMBL: AK006582; BAB24660.1;
 DR MGD; MGI:1920566; Calr3.
 DR InterPro; IPR009033; Calret_calmex_P.
 DR InterPro; IPR001580; Calreticulin.
 DR InterPro; IPR008985; ConA-like lec_gl.
 DR InterPro; IPR000886; ER_target_S.
 DR Pfam; PF00262; calreticulin; 1.
 DR PIRSF; PIRSF002356; Calreticulin; 1.
 DR PRINTS; PR00626; CALRETICULIN.
 DR ProDom; PD001866; Calreticulin; 1.
 DR ProSITE; PS00803; CALRETICULIN_1; 1.
 DR ProSITE; PS00804; CALRETICULIN_2; 1.
 DR ProSITE; PS00014; ER_TARGET; FALSE NEG.
 DR Chaperone; Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
 KW SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 380
 FT DOMAIN 20 197
 FT DOMAIN 198 291
 FT DOMAIN 292 380
 FT DOMAIN 191 246
 FT REPEAT 191 202
 FT REPEAT 191 202

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FT REPEAT 209 220 1-2.
FT REPEAT 222 231 1-3.
FT REPEAT 235 246 1-4.
FT DOMAIN 250 280 3 X APPROXIMATE REPEATS.
FT REPEAT 250 256 2-1.
FT REPEAT 260 268 2-2.
FT REPEAT 270 280 2-3.
FT SITE 377 380 PREVENT SECRETION FROM ER (POTENTIAL).
FT DISULFID 137 163 BY SIMILARITY.
FT CARBOHYD 42 42 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 201 201 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 380 AA; 44197 MW; B13BC4ADB1B0442 CRC64;

Query Match 57.0%; Score 147; DB 1; Length 380;
Best Local Similarity 69.2%; Pred. No. 1.7e-11; Indels 0; Gaps 0;
Matches 27; Conservative 5; Mismatches 7;

QY 11 KDRCRCKDDETHLYTVLRPDNTYEVKIDNSQVSGSLE 49
Db 159 KPIRCVKDGTHTLYTLRLPDLSEYVKVDQSQSIESGSIE 197

RESULT 15
CRT3 HUMAN
ID CRT3 HUMAN STANDARD; PRT; 384 AA.
AC Q96L12; Q96L13;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Calreticulin 3 precursor (calreticulin 2).
GN CALR3 OR CRT2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
TISSUE=Testis;
RA Ishibashi T., Kanehori K., Yosida M., Watanabe S., Ishida S., Ono Y.,
RA Hecuta T., Hiraoka S., Murakawa K., Takiguchi S., Kusano J.,
RA Watanabe M., Fujimori K., Tanai H., Ishida M., Yamashita H., Chiba Y.,
RA Suzuki Y., Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M.,
RA Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A.,
RA Kawakami B., Nagai K., Isogai T., Sugano S.;
RA "NEDO human cDNA sequencing project";
RA Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
[2]
SEQUENCE FROM N.A.
TISSUE=Testis;
RC MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[3]
IDENTIFICATION, AND TISSUE SPECIFICITY.
RN MEDLINE=22271577; PubMed=12384296;
RX

```

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RA Persson S., Rosenquist M., Sommarin M.;
RT "Identification of a novel calreticulin isoform (Crt2) in human and
RT mouse.";
RL Gene 297:151-158 (2002).
CC -!- FUNCTION: Ca(2+)-binding chaperone (By similarity). (By similarity).
CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen
CC -!- TISSUE SPECIFICITY: Testis specific.
CC -!- SIMILARITY: Belongs to the calreticulin family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AK058084; BAB71655.1; -
CC EMBL; BC014595; AAH14595.1; -
CC GenBank; HGNC:20407; CALR3.
DR InterPro; IPR009033; Calret calnex P.
DR InterPro; IPR001580; Calreticulin_
DR InterPro; IPR008985; ConA-like lec_gl.
DR InterPro; IPR000886; ER_target_S.
DR Pfam; PF00262; calreticulin; 1.
DR PIRSF; PIRSF002356; Calreticulin.
DR PRINTS; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00014; ER_TARGET; 1.
KW Chaperone; Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 384 CALRETICULIN 3.
FT DOMAIN 20 197 N-DOMAIN.
FT DOMAIN 198 294 P-DOMAIN.
FT DOMAIN 295 384 C-DOMAIN.
FT DOMAIN 191 245 4 X APPROXIMATE REPEATS.
FT REPEAT 191 202 1-1.
FT REPEAT 208 219 1-2.
FT REPEAT 221 230 1-3.
FT REPEAT 234 245 1-4.
FT DOMAIN 249 283 3 X APPROXIMATE REPEATS.
FT REPEAT 249 259 2-1.
FT REPEAT 263 271 2-2.
FT REPEAT 273 283 2-3.
FT DOMAIN 357 362 POLY-GLU.
FT SITE 381 384 PREVENT SECRETION FROM ER (POTENTIAL).
FT DISULFID 137 163 BY SIMILARITY.
FT CARBOHYD 42 42 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 201 201 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 8 8 F >> L (IN REF. 1).
SQ SEQUENCE 384 AA; 45029 MW; 33F7CB523FEFF187 CRC64;

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Query Match 56.2%; Score 145; DB 1; Length 384;
 Best Local Similarity 59.2%; Pred. No. 3e-11;
 Matches 29; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

QY 1 NYGKQVNLKDKIRCKDDETHLYTVLRPDNTYEVKIDNSQVSGSLE 49
 Db 149 HFKNKYHENKLIIRCKVDGTHTLYTLRLPDLSEYVKVDQSQSIESGSIE 197

Search completed: October 4, 2004, 13:04:01
 Job time : 7.20588 secs

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GenCore version 5.1.6
Copyright (C) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 4, 2004, 12:52:42 ; Search time 29.6882 Seconds
(without alignments)
520.758 Million cell updates/sec

Title: US-09-807-148-6
Perfect score: 258
Sequence: 1 NYGKNVLRINKDKDEF.....PDNTYEVKIDNSQVESGSLE 49

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues
Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPREMBL 25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Result No.	Score	Query Match	Length	ID	Description
1	234	90.7	318	13 Q9PTX7	Q9ptx7 lampetra re
2	226	87.6	343	13 Q91711	Q91711 xenopus lae
3	226	87.6	411	13 Q91710	Q91710 xenopus lae
4	226	87.6	413	13 Q7ZWU8	Q7zwu8 xenopus lae
5	226	87.6	418	13 Q7ZXV3	Q7zxv3 xenopus lae
6	221	85.7	405	5 Q26268	Q26268 aplysia cal
7	217	84.1	403	5 Q81S63	Q81s63 cotesia rub
8	215	83.3	407	5 Q86G72	Q86g72 dermacentor
9	215	83.3	417	13 Q9PUC1	Q9puc1 brachydanio
10	212	82.3	423	13 Q7SZM3	Q7szm3 ictalurid p
11	211	81.8	406	5 Q8WR36	Q8wr36 anopheles g
12	210	81.4	417	13 Q802X3	Q802x3 brachydanio
13	210	81.4	419	13 Q89894	Q89894 rana rugosa
14	210	81.4	421	5 Q9U6S0	Q9u6s0 strongyloce
15	209	81.0	406	5 Q9U916	Q9u916 drosophila
16	209	81.0	411	5 Q8MW23	Q8mw23 boophilus m

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	234	90.7	318	13 Q9PTX7	Q9ptx7 lampetra re
2	226	87.6	343	13 Q91711	Q91711 xenopus lae
3	226	87.6	411	13 Q91710	Q91710 xenopus lae
4	226	87.6	413	13 Q7ZWU8	Q7zwu8 xenopus lae
5	226	87.6	418	13 Q7ZXV3	Q7zxv3 xenopus lae
6	221	85.7	405	5 Q26268	Q26268 aplysia cal
7	217	84.1	403	5 Q81S63	Q81s63 cotesia rub
8	215	83.3	407	5 Q86G72	Q86g72 dermacentor
9	215	83.3	417	13 Q9PUC1	Q9puc1 brachydanio
10	212	82.3	423	13 Q7SZM3	Q7szm3 ictalurid p
11	211	81.8	406	5 Q8WR36	Q8wr36 anopheles g
12	210	81.4	417	13 Q802X3	Q802x3 brachydanio
13	210	81.4	419	13 Q89894	Q89894 rana rugosa
14	210	81.4	421	5 Q9U6S0	Q9u6s0 strongyloce
15	209	81.0	406	5 Q9U916	Q9u916 drosophila
16	209	81.0	411	5 Q8MW23	Q8mw23 boophilus m

ALIGNMENTS

RESULT 1

Q9PTX7 PRELIMINARY; PRT; 318 AA.

AC Q9PTX7; 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Calreticulin (fragment).

OS Lampetra reissneri (Far Eastern brook lamprey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;

OC Petromyzontiformes; Petromyzontidae; Lethenteron.

OX NCBI_TaxID=7753;

RN [1] SEQUENCE FROM N.A.

RP MEDLINE=2063780; PubMed=10594174; Kuraku S., Hoshiyama D., Katoh K., Suga H., Miyata T.; "Monophyly of lampreys and hagfishes supported by nuclear DNA-coded genes." J. Mol. Evol. 49:729-735(1999).

RL EMBL; AB025328; BAA89481.1; GO; GO:0005514; F:calcium ion storage activity; IEA. InterPro; IPR001580; Calreticulin. InterPro; IPR009033; Calreticulin. InterPro; IPR009885; ConA-like lec_gl. InterPro; IPR000886; ER target_S. Pfam; PF00362; calreticulin_1. PRINIS; PR00626; CALRETICULIN. ProDom; PD001866; Calreticulin. PROSITE; PS00804; CALRETICULIN_2; 1. PROSITE; PS00805; CALRETICULIN_REPEAT; 3. PROSITE; PS00014; ER TARGET; 1. NON_TER 1. FT NON TER 1. SQ SEQUENCE 318 AA; 36997 MW; C88102EA1CAC1506 CRC64;

Query Match 90.7%; Score 234; DB 13; Length 318;
Best local similarity 89.8%; Pred. No. 2.7e-21;
Matches 44; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 NYGKNVLRINKDKDEFTHLYTLVRPDNTYEVKIDNSQVESGSLE 49

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Db      48  NYGQKHLINKDCKODEYTHLYTLVRPDQTYEVKIDNKKVSGSLE 96
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
RESULT 2
Q91711 PRELIMINARY; PRT; 343 AA.
ID Q91711 AC Q91711
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Calreticulin (Fragment).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CNS;
RA Treves S., Zorzato F., Pozzan T.;
RL "Identification of calreticulin isoform in the CNS.";
RT Biochem. J. 0:0-0(0).
DR EMBL; X67598; CAA47867.1; -.
DR PIR; S29130; S29130
DR GO; GO:0005514; F:calcium ion storage activity; IEA.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR009033; Calret_calmex.P.
DR InterPro; IPR008985; ConA_like_lcc_gl.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
DR NON_TER
FT NON_TER
SQ SEQUENCE 343 AA; 401.05 MW; 3E7DDAFA39B91DE1 CRC64;

Query Match 87.6%; Score 226; DB 13; Length 343;
Best Local Similarity 89.6%; Pred. No. 3e-20;
Matches 43; Conservative 2; Mismatches 3; Indels 0;

QY 2 YGKQVLNKIDRKDBEFTHLYTLVRPDNTYEVKIDNSQVESGSLE 49
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      122  YKKQLNKIDRKDBSFTHLYTLVRPDNTYEVKIDNSQVESGSLE 169
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

RESULT 3
Q91710 PRELIMINARY; PRT; 411 AA.
ID Q91710 AC Q91710
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Calreticulin precursor (Fragment).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CNS;
RA Treves S., Zorzato F., Pozzan T.;
RL "Identification of calreticulin isoform in the CNS.";
RT Biochem. J. 0:0-0(0).
DR EMBL; X67597; CAA47866.1; -.
DR PIR; S29129; S29129.
DR GO; GO:0005514; F:calcium ion storage activity; IEA.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR009033; Calret_calmex.P.
DR InterPro; IPR008985; ConA_like_lcc_gl.
DR InterPro; IPR00886; ER target S.

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DR	Pfam; PF00262; calreticulin; 1.
DR	PRINTS; PR00626; CALRETICULIN.
DR	ProDom; PD001866; Calreticulin; 1.
DR	PROSITE; PS00803; CALRETICULIN_1; 1.
DR	PROSITE; PS00804; CALRETICULIN_2; 1.
DR	PROSITE; PS00805; CALRETICULIN_REPEAT; 2.
DR	PROSITE; PS00014; ER_TARGET; 1.
KW	Signal
FT	NON_TER
FF	SIGNAL
FT CHAIN	<1
FF SIGNAL	12
FT CHAIN	13
FF SIGNAL	411
SEQUENCE	411 AA; 48344 MW; 891DA6GE0DEBSEFA CRC64;
Query Match	87.6%; Score 226; DB 13; Length 411;
Best Local Similarity	89.6%; Pred.No.3.7e-20;
Matches	43; Conservative 2; Mismatches 3; Indels 0;
OY	2 YKGXVLIINKDIRCKDDETHLYTLIVRPDNTVEVKIDNSQVESGSLE 49 :
DB	145 YKKNLQIINKDIRCKDDSTHLYTLIVRPDNTVEVKIDNSQVESGSLE 192 :
RESULT 4	
Q7ZWU8	
IID Q7ZNU8	PRELIMINARY; PRT; 413 AA.
AC Q7ZNU8	
DT 01-JUN-2003	(TrEMBLrel. 24, Created)
DT 01-JUN-2003	(TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003	(TrEMBLrel. 25, Last annotation update)
DE	Similar to calreticulin.
OS Xenopus laevis	(African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;	
OC Xeropodinae; Xenopus.	
OX NCBI_taxid=8355;	
RN [1]	
RP SEQUENCE FROM N.A.	
RRC TISSUE=Embryo;	
RCA Klein S.; Strausberg R.;	
RRL Submitted (FEB-2003) to the EMBL/GenBank/DDJB databases.	
RRL EMBL; BC046699; AH46699.1; "	
DR GO; GO:0005514; F.calcium ion storage activity; IEA.	
DR Interpro; IPRO01580; Calreticulin.	
DR Interpro; IPRO09033; Calret_calmex.P.	
DR Interpro; IPRO08985; ConA_like lec_gl.	
DR Interpro; IPRO00885; ER_target_S.	
DR Pfam; PF00262; calreticulin; 1.	
DR PRINTS; PR00626; CALRETICULIN.	
DR ProDom; PD001866; Calreticulin; 1.	
DR PROSITE; PS00803; CALRETICULIN_1; 1.	
DR PROSITE; PS00804; CALRETICULIN_2; 1.	
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.	
DR PROSITE; PS00014; ER_TARGET; 1.	
SEQUENCE	413 AA; 48521 MW; DE002PFG0523772B CRC64;
Query Match	87.6%; Score 226; DB 13; Length 413;
Best Local Similarity	89.6%; Pred.No.3.7e-20;
Matches	43; Conservative 2; Mismatches 3; Indels 0;
OY	2 YKGXVLIINKDIRCKDDETHLYTLIVRPDNTVEVKIDNSQVESGSLE 49 :
DB	151 YKKNLQIINKDIRCKDDSTHLYTLIVRPDNTVEVKIDNSQVESGSLE 198 :
RESULT 5	
Q7ZXV3	
IID Q7ZXY3	PRELIMINARY; PRT; 418 AA.
AC Q7ZXY3	
DT 01-JUN-2003	(TrEMBLrel. 24, Created)
DT 01-JUN-2003	(TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003	(TrEMBLrel. 25, Last annotation update)
DE	Similar to calreticulin.
OS Xenopus laevis	(African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodidae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.

RC TISSUE=Embryo;
 RC Klein S., Strausberg R.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 RL EMBL; BC044068; AAF44068.1;
 DR GO; GO:0005514; F:calcium ion storage activity; IEA.
 DR InterPro; IPR001580; Calreticulin.
 DR InterPro; IPR009033; Calret calnex P.
 DR InterPro; IPR008985; ConA like lec_gl.
 DR InterPro; IPR000886; ER_target_S.
 DR Pfam; PF00262; calreticulin; 1.
 DR PRINTS; PR00626; CALRETICULIN.
 DR ProDom; PD001866; Calreticulin; 1.
 DR PROSITE; PS00803; CALRETICULIN_1; 1.
 DR PROSITE; PS00804; CALRETICULIN_2; 1.
 DR PROSITE; PS00805; CALRETICULIN_REPEAT; 2.
 DR PROSITE; PS00014; ER_TARGET; 1.
 DR PROSITE; PS00014; ER_TARGET; 1.
 SQ SEQUENCE 418 AA; 49028 MW; 731C1C9AA0BF9A53 CRC64;

Query Match 87.6%; Score 226; DB 13; Length 418;
 Best Local Similarity 89.6%; Pred. No. 3.7e-20;
 Matches 43; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 YKGNVLIKIDCKDDEFTHTLTVLRPDNTYEVKIDNSQVSGSLE 49
 DB 151 YKKNQLQIKDCKDDEFTHTLTVLRPDNTYEVKIDNSQVSGSLE 198

RESULT 6

Q26268
 ID Q26268 PRELIMINARY; PRT; 405 AA.
 AC Q26268
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Calreticulin.
 GN CALRETICULIN.
 OS Aplysia californica (California sea hare).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 OC Apogastropoda; Heterobranchia; Euthyneura; Opisthobranchia; Anaspidae;
 OC Aplysioidea; Aplysiidae; Aplysia.
 OX NCBI_TaxID=6500;
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE=93098937; PubMed=1463604;
 RA Kennedy T.E., Kuhl D., Barzilai A., Sweatt J.D., Kandel E.R.;
 RT "Long-term sensitization training in Aplysia leads to an increase in
 RT calreticulin, a major presynaptic calcium-binding protein.";
 RL Neuron 9:1013-1024(1992).
 DR EMBL; S51239; AAS24569.1;
 DR PIR; JH0795; JH0795.
 DR GO; GO:0005514; F:calcium ion storage activity; IEA.
 DR InterPro; IPR001580; Calreticulin.
 DR InterPro; IPR009033; Calret calnex P.
 DR InterPro; IPR008985; ConA like lec_gl.
 DR InterPro; IPR000886; ER_target_S.
 DR Pfam; PF00262; calreticulin; 1.
 DR PRINTS; PR00626; CALRETICULIN.
 DR ProDom; PD001866; Calreticulin; 1.
 DR PROSITE; PS00803; CALRETICULIN_1; 1.
 DR PROSITE; PS00804; CALRETICULIN_2; 1.
 DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
 DR PROSITE; PS00014; ER_TARGET; 1.
 DR PROSITE; PS00014; ER_TARGET; 1.
 SQ SEQUENCE 405 AA; 46738 MW; 14CAA201840D1D69 CRC64;

Query Match 85.7%; Score 221; DB 5; Length 405;
 Best Local Similarity 81.6%; Pred. No. 1.5e-19;
 Matches 40; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

OY 1 NYKGNVLIKIDCKDDEFTHTLTVLRPDNTYEVKIDNSQVSGSLE 49
 DB 145 NYKGNVLIKIDCKDDEFTHTLTVLRPDNTYEVKIDNSQVSGSLE 193

RESULT 7

Q81S63
 ID Q81S63 PRELIMINARY; PRT; 403 AA.
 AC Q81S63
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Calreticulin.
 OS Cotesia rubecula.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Ichneumonidae;
 OC Braconidae; Microgasterinae; Cotesia.
 OX NCBI_TaxID=32392;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Asgari S., Zhang G., Schmidt O.;
 RA "polydnavirus particle proteins with similarities to molecular
 RT chaperons, heat shock protein 70 and calreticulin.";
 RT Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.

RL EMBL; AY150370; AAN73309.1;
 DR GO; GO:0005514; F:calcium ion storage activity; IEA.
 DR InterPro; IPR001580; Calreticulin.
 DR InterPro; IPR009033; Calret calnex P.
 DR InterPro; IPR008985; ConA like lec_gl.
 DR InterPro; IPR000886; ER_target_S.
 DR Pfam; PF00262; calreticulin; 1.
 DR PRINTS; PR00626; CALRETICULIN.
 DR ProDom; PD001866; Calreticulin; 1.
 DR PROSITE; PS00803; CALRETICULIN_1; 1.
 DR PROSITE; PS00804; CALRETICULIN_2; 1.
 DR PROSITE; PS00805; CALRETICULIN_REPEAT; 2.
 DR PROSITE; PS00014; ER_TARGET; 1.
 DR PROSITE; PS00014; ER_TARGET; 1.
 SQ SEQUENCE 403 AA; 46550 MW; 259D771A822DB126 CRC64;

Query Match 84.1%; Score 217; DB 5; Length 403;
 Best Local Similarity 81.6%; Pred. No. 4.9e-19;
 Matches 40; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

OY 1 NYKGNVLIKIDCKDDEFTHTLTVLRPDNTYEVKIDNSQVSGSLE 49
 DB 148 NYKGNVLIKIDCKDDEFTHTLTVLRPDNTYEVKIDNSQVSGSLE 196

RESULT 8

Q86G72
 ID Q86G72 PRELIMINARY; PRT; 407 AA.
 AC Q86G72
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Calreticulin.
 OS Dermacentor variabilis.
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
 OC Parasitiformes; Ixodida; Ixodidae; Dermacentor.
 OX NCBI_TaxID=34621;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Simser J.A., Mulenga A., Macaluso K.R., Azad A.F.;
 RA "Molecular characterization of Dermacentor variabilis calreticulin.";
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.

RL EMBL; AY241957; AAC92278.1;
 DR GO; GO:0005514; F:calcium ion storage activity; IEA.
 DR InterPro; IPR001580; Calreticulin.
 DR InterPro; IPR009033; Calret calnex P.
 DR InterPro; IPR008985; ConA like lec_gl.
 DR InterPro; IPR000886; ER_target_S.
 DR Pfam; PF00262; calreticulin; 1.

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DR PRINTS; PRO0626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
DR PROSITE; PS00014; ER_TARGET; 1.
SQ SEQUENCE 407 AA; 47190 MW; FFE8063AC49446E8 CRC64;

Query Match      83.3%; Score 215; DB 5; Length 407;
Best Local Similarity 81.6%; Pred. No. 8.9e-19;
Matches 40; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 NYKGNVLINKDKDDDETHLYTLIVRPDNTYEVKIDNSQVSGSLE 49
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 148 NYKGNHLINKDKDDVDFHLYTLIVRPDNTYQVKIDNVVKGGELE 196

RESULT 9
Q9PUC1 ID Q9PUC1 PRELIMINARY; PRT; 417 AA.
AC Q9PUC1
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Calreticulin.
GN CALR
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20190113; PubMed=10660676;
RA Rubinstein A.L.; Lee D.; Luo R.; Henion P.D.; Halpern M.E.;
RT "Genes dependent on zebrafish cyclops function identified by AFLP
RT differential gene expression screen.";
RL Genesis 26:86-97(2000).
DR EMBL; AF195882; RA13700.1; -.
DR ZFIN; ZDB-GENE-000208-17; calr.
DR GO; GO:0005514; F:calcium ion storage activity; IEA.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR009033; Calret_cainex_P.
DR InterPro; IPR008985; ConA_like lec_gl.
DR InterPro; IPR000886; ER_target_S_g1.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
DR PROSITE; PS00014; ER_TARGET; 1.
SQ SEQUENCE 417 AA; 48723 MW; 2000C5B4004699B6 CRC64;

Query Match      83.3%; Score 215; DB 13; Length 417;
Best Local Similarity 81.6%; Pred. No. 9.1e-19;
Matches 40; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 NYKGNVLINKDKDDDETHLYTLIVRPDNTYEVKIDNSQVSGSLE 49
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 149 NYKGNHLINKDKDDVDFHLYTLIVRPDNTYQVKIDNVVKGGELE 197

RESULT 10
Q7SZM3 ID Q7SZM3 PRELIMINARY; PRT; 423 AA.
AC Q7SZM3
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE ER-resident chaperone calreticulin.
OS Ictalurus punctatus (Channel catfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
OC Ictaluridae; Ictalurus.
OX NCBI_TaxID=7998;
RN [1]
RP SEQUENCE FROM N.A.
RA McConnell T.J.; Pitzer J.E.;
RT "Calreticulin in the Channel Catfish, Ictalurus punctatus.";
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY342298; AAQ19852.1; -.
SQ SEQUENCE 423 AA; 49186 MW; ED7CBA5C1FBC07EB CRC64;

Query Match      82.2%; Score 212; DB 13; Length 423;
Best Local Similarity 81.6%; Pred. No. 2.2e-18;
Matches 40; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 NYKGNVLINKDKDDDETHLYTLIVRPDNTYEVKIDNSQVSGSLE 49
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 149 NYKGNHLINKDKDDDETHLYTLIVRPDNTYQVKIDNVVKGGELE 197

RESULT 11
Q8WR36 ID Q8WR36 PRELIMINARY; PRT; 406 AA.
AC Q8WR36
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Calreticulin.
OS Anopheles gambiae (African malaria mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
OX NCBI_TaxID=7165;
RN [1]
RP SEQUENCE FROM N.A.
RA Francischetti I.M.; Valenzuela J.G.; Ribeiro J.M.;
RT "Towards a catalog for genes and proteins from the salivary gland of
RT the malaria vector, Anopheles gambiae.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF457551; AAL68781.1; -.
DR GO; GO:0005514; F:calcium ion storage activity; IEA.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR009033; Calret_cainex_P.
DR InterPro; IPR008985; ConA_like lec_gl.
DR InterPro; IPR000886; ER_target_S.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
DR PROSITE; PS00014; ER_TARGET; 1.
SQ SEQUENCE 406 AA; 46285 MW; 85068FBBCA9931F1 CRC64;

Query Match      81.8%; Score 211; DB 5; Length 406;
Best Local Similarity 81.6%; Pred. No. 2.8e-18;
Matches 40; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 NYKGNVLINKDKDDDETHLYTLIVRPDNTYEVKIDNSQVSGSLE 49
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 146 SYKGNHLINKDKDDVDFHLYTLIVRPDNTYEVKIDNVVKGGELE 194

RESULT 12
Q802X3 ID Q802X3 PRELIMINARY; PRT; 417 AA.
AC Q802X3
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to calreticulin.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;

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Best Local Similarity 81.6%; Pred. No. 3.9e-18; Mismatches 4; Indels 0; Gaps 0;
Matches 40; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 NYKGNVLIKKDKCKDDETHLYTLVIRPDNTYEVKIDNSQVSGSLE 49
DB 150 NYKGNLIKKDKCKDDETHLYTLVIRPDNTYEVKIDNSQVSGSLE 198

RESULT 14
Q9U916 PRELIMINARY; PRT; 421 AA.
AC Q9U916
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Calreticulin precursor.
GN CALRET.
OS Strongylocentrotus purpuratus (Purple sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinozoa; Echinacea; Echinoidea; Strongylocentrotidae;
OC Strongylocentrotus.
OC NCBI_TaxID=7668;
RN [1]
RP SEQUENCE FROM N.A.
RA Susan J.M., Just M.L., Lennarz W.J.;
RT "Cloning and Characterization of Alphas Integrin and Calreticulin in
RT Embryos of the Sea Urchin."
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF177915; AAD55725.1;
DR GO; GO:0005514; F:calcium ion storage activity; IEA.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR009033; Calret calnex P.
DR InterPro; IPR008985; ConA-like lec_gl.
DR InterPro; IPR00886; ER_target_S.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR PROSITE; PS00804; CALRETICULIN; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
DR PROSITE; PS00014; ER_TARGET; 1.
KW Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 421 CALRETICULIN.
SQ SEQUENCE 421 AA; 48822 MW; 172C664F59F41F93 CRC64;

Query Match 81.4%; Score 210; DB 5; Length 421;
Best Local Similarity 75.5%; Pred. No. 3.9e-18; Mismatches 4; Indels 0; Gaps 0;
Matches 37; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 1 NYKGNVLIKKDKCKDDETHLYTLVIRPDNTYEVKIDNSQVSGSLE 49
DB 148 NYKGNLIKKDKCKDDETHLYTLVIRPDNTYEVKIDNSQVSGSLE 196

RESULT 15
Q9U916 PRELIMINARY; PRT; 406 AA.
AC Q9U916
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Calreticulin.
GN CRC OR CG9429.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
CN NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Dodo K., Sakoyama Y., Gamo S.;
RT STRAIN=OREGON-R;
RA "Drosophila melanogaster calreticulin for mRNA.";

Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC046906; AA46906.1;
DR GO; GO:0005514; F:calcium ion storage activity; IEA.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR009033; Calret calnex P.
DR InterPro; IPR008985; ConA-like lec_gl.
DR InterPro; IPR00886; ER_target_S.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR PROSITE; PS00804; CALRETICULIN; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
DR PROSITE; PS00014; ER_TARGET; 1.
SQ SEQUENCE 417 AA; 48259 MW; F7D11614F4319586 CRC64;

Query Match 81.4%; Score 210; DB 13; Length 417;
Best Local Similarity 79.6%; Pred. No. 3.9e-18; Mismatches 6; Indels 0; Gaps 0;
Matches 39; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 NYKGNVLIKKDKCKDDETHLYTLVIRPDNTYEVKIDNSQVSGSLE 49
DB 150 NYKGNLIKKDKCKDDETHLYTLVIRPDNTYEVKIDNSQVSGSLE 198

RESULT 13
Q98984 PRELIMINARY; PRT; 419 AA.
AC Q98984
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Calreticulin.
OS Rana rugosa (Wrinkled frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.
OX NCBI_TaxID=8410;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=96234004; PubMed=8654561;
RA Yamamoto S., Nakamura M.;
RT "Calnexin: its molecular cloning and expression in the liver of the
RT frog, Rana rugosa."
RL FEBS Lett. 387:27-32(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=96387817; PubMed=8795287;
RA Yamamoto S., Kondo Y., Hanada H., Nakamura M.;
RT "Strong expression of the calreticulin gene in the liver of Rana
RT rugosa tadpoles, but not adult frogs."
RL J. Exp. Zool. 275:431-443(1996).
DR EMBL; D78589; BAAL1425.1;
DR PIR; S71343; S71343.
DR GO; GO:0005514; F:calcium ion storage activity; IEA.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR009033; Calret calnex P.
DR InterPro; IPR008985; ConA-like lec_gl.
DR InterPro; IPR00886; ER_target_S.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR PROSITE; PS00804; CALRETICULIN; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
DR PROSITE; PS00014; ER_TARGET; 1.
SQ SEQUENCE 419 AA; 48658 MW; 2C857036769673BF CRC64;

Query Match 81.4%; Score 210; DB 13; Length 419;

Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.

EMBL; AB000718; EAA85379.1; -.
FlyBase; Fgn0005585; Crc.
GO; GO:0007417; P:central nervous system development; IMP
InterPro; IPR001580; Calreticulin.
InterPro; IPR009033; Calret calnex P.
InterPro; IPR008985; ConA like lec_gl.
InterPro; IPR008886; ER target_S_gl.
Pfam; PF00262; calreticulin; 1.
PRINTS; P00626; CALRETICULIN.
ProDom; PD001866; Calreticulin; 1.
PROSITE; PS00803; CALRETICULIN 1; 1.
PROSITE; PS00804; CALRETICULIN 2; 1.
PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
PROSITE; PS00014; ER_TARGET; 1.
SEQUENCE 406 AA; 46809 MW; 658BA49AGB81CC427 CRC64;
SQ

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Query March      81.0%  Score 203;  DB 5;  Length 406;
Best Local Similarity 79.6%  Pres. NO. 5.1e-18;
Matches 39;  Conservative 5;  Mismatches 5;  Indels 0;  Gaps 0;

Oy 1 NYGKNVLNKRICKDDFFHTLYTLIVRPDNTYEVKIDNSQVFSGLIE 49
    : : : : :
Db 149 SYGKNHLISKIRCKDDVYTFHTLYTLIVRPDNTYEVLDNKEVSGNLE 197
    : : : : :

```

Search completed: October 4, 2004, 13:05:52
Job time : 29.6882 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 4, 2004, 12:52:42 ; Search time 36.3529 Seconds
(without alignments)
520.758 Million cell updates/sec

Title: US-09-807-148-8
Perfect score: 318
Sequence: 1 GPCTKKVHVIFNYKGRNLI.....PNTYEVKIDNSQVSGSL 60

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 31518202 residues
Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPREMBL 25:*

- 1: sp_archea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mbc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	294	92.5	318	13	Q9PTX7	Q9PTX7 lampetra re
2	281	88.4	405	5	Q26268	Q26268 aphysia cal
3	278	87.4	343	13	Q91711	Q91711 xenopus lae
4	278	87.4	411	13	Q91710	Q91710 xenopus lae
5	278	87.4	413	13	Q72WD8	Q72WD8 xenopus lae
6	278	87.4	418	13	Q72XY3	Q72XY3 xenopus lae
7	276	86.8	403	5	Q81S63	Q81S63 cotesia rub
8	275	86.5	407	5	Q86G72	Q86G72 dermaceator
9	271	85.2	406	5	Q8WR36	Q8WR36 anopheles g
10	270	84.9	421	5	Q9U6S0	Q9U6S0 strongyloce
11	269	84.6	406	5	Q9U916	Q9U916 drosophila
12	268	84.3	398	5	Q869E0	Q869E0 bombyx mori
13	268	84.3	398	5	Q721E6	Q721E6 bombyx mori
14	267	84.0	397	5	Q8WPG8	Q8WPG8 galleria me
15	267	84.0	410	5	Q16893	Q16893 amblyomma a
16	265	83.3	407	5	Q8T9U3	Q8T9U3 aedes aegypt

17	265	83.3	411	5	Q8MWP3	Q8MWP3 boophilus m
18	262	82.4	419	13	Q98984	Q98984 rana rugosa
19	259	81.4	417	13	Q9PUC1	Q9PUC1 brachydanio
20	256	80.5	423	13	Q7SZM3	Q7SZM3 ictalurus p
21	254	79.9	417	13	Q802X3	Q802X3 brachydanio
22	249	78.3	387	5	Q97372	Q97372 dirofilaria
23	248	78.0	415	5	Q8WRU9	Q8WRU9 meloidosyne
24	243	76.4	375	5	O18478	O18478 litomosoid
25	240.5	75.6	403	5	O76961	O76961 nicator ame
26	237	74.5	350	5	Q26514	Q26514 schistosoma
27	237	74.5	396	5	O45034	O45034 schistosoma
28	217	68.2	321	13	Q9USG0	Q9USG0 eptatretus
29	209	65.7	395	5	Q96722	Q96722 taenia soli
30	179	56.3	421	10	Q43712	Q43712 zea mays (m
31	179	56.3	442	10	Q7Y140	Q7Y140 oryza sativ
32	177	55.7	321	10	Q41799	Q41799 zea mays (m
33	176	55.3	412	10	Q40040	Q40040 hordeum vul
34	176	55.3	415	10	Q40041	Q40041 hordeum vul
35	174.5	54.9	427	10	Q9FYV2	Q9FYV2 pinus taeda
36	174	54.7	425	10	Q8LJ85	Q8LJ85 oryza sativ
37	173	54.4	137	11	Q9D373	Q9D373 mus musculu
38	173	54.4	272	11	Q8BL82	Q8BL82 mus musculu
39	172	54.1	416	10	Q8H792	Q8H792 arabidopsis
40	169	53.1	240	10	Q9ST29	Q9ST29 solanum mel
41	169	53.1	389	10	Q40567	Q40567 nicotiana t
42	169	53.1	424	10	Q94AW7	Q94AW7 arabidopsis
43	169	53.1	424	10	Q8LC80	Q8LC80 arabidopsis
44	168	52.8	422	10	Q22502	Q22502 brassica na
45	167	52.5	380	10	Q7XAB5	Q7XAB5 brassica ra

ALIGNMENTS

RESULT 1

Q9PTX7 PRELIMINARY; PRT; 318 AA.
ID Q9PTX7
AC Q9PTX7
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DI 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Calreticulin (Fragment).
OS Lampetra reissneri (Far Eastern brook lamprey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC Petromyzontiformes; Petromyzontidae; Lethenteron.
CX NCBI_TaxID=7753;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2063750; PubMed=10594174;
RA Kuraku S., Hoshiyama D., Katoh K., Suga H., Miyata T.i
RT "Monophyly of lampreys and hagfishes supported by nuclear DNA-coded
RT genes.";
RL J. Mol. Evol. 49:729-735(1999).
DR EMBL; AB025328; BAA88481.1; .
DR GO; GO:0005514; F:calcium ion storage activity; IEA.
DR InterPro; IPR001590; Calreticulin.
DR InterPro; IPR009033; Calreticulin_P.
DR InterPro; IPR008985; ConA_like_rec_gi.
DR InterPro; IPR000886; ER_target_S.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
DR PROSITE; PS00014; ER_TARGET; 1.
FT NON_TER
SQ SEQUENCE 318 AA; 36997 MW; C88102EALCACL506 CRC64;

Query Match 92.5%; Score 294; DB 13; Length 318;

Best Local Similarity 91.7%; Pred. No. 1.3e-26;

Matches 55; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Oy 1 GPCTKKVHVIFNYKGRNLIKDRCODEFTHLYTLIVRPDNTYEVKIDNSQVSGSL 60

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Db 37 GPGTKKVHVFYKGNLKNKDIRCKDDYTHLYTLIVRPDQTYEVKIDNKVSGSLE 96
|||||
RESULT 2
Q26268 PRELIMINARY; PRT; 405 AA.
AC Q26268;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Calreticulin.
GN CALRETICULIN.
OS Aplysia californica (California sea hare).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Heterobranchia; Euthyneura; Opisthobranchia; Anaspidea;
OC Aplysioidea; Aplysiidae; Aplysia.
OC NCBI_TaxID=6500;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9309937; PubMed=1463604;
RA Kennedy T.E., Kuhl D., Barzilai A., Sweatt J.D., Kandel E.R.;
RT "Long-term sensitization training in Aplysia leads to an increase in
RL calreticulin, a major presynaptic calcium-binding protein.";
DR Neuron 9:1013-1024(1992).
DR EMBL; S51239; AAB24569.1; -.
DR PIR; JH0795; JH0795.
DR GO; GO:0005514; F:calcium ion storage activity; IEA.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR009033; Calret. calnex.P.
DR InterPro; IPR008985; ConA like lec_gl.
DR InterPro; IPR000886; ER target_S.
DR Pfam; PF00262; calreticulin_1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
DR SQ SEQUENCE 405 AA; 46738 MW; 14CAA201840D1D69 CRC64;

Query Match 88.4%; Score 281; DB 5; Length 405;
Best Local Similarity 85.0%; Pred. No. 5.7e-25;
Matches 51; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 GPGTKKVHVFYKGNLKNKDIRCKDDYTHLYTLIVRPDQTYEVKIDNKVSGSLE 60
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Db 134 GPGTKKVHVFYKGNLKNKDIRCKDDVFSHLYTLIVRPDNTYEVKIDNKVSGDLE 193
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RESULT 3
Q91711 PRELIMINARY; PRT; 343 AA.
AC Q91711;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Calreticulin (Fragment).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OC NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=CNS;
RA Treves S., Zorzato F., Pozzan T.;
RT "Identification of calreticulin isoform in the CNS.";
RL Biochem. J. 0:0-0(0).
DR EMBL; X67598; CAA47867.1; -.
DR PIR; S29130; S29130.
DR GO; GO:0005514; F:calcium ion storage activity; IEA.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR009033; Calret. calnex.P.
DR InterPro; IPR008985; ConA like lec_gl.
DR InterPro; IPR000886; ER target_S.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 2.
DR SQ SEQUENCE 411 AA; 48344 MW; 891DA66E00EBBEFA CRC64;

Query Match 87.4%; Score 278; DB 13; Length 411;
Best Local Similarity 88.3%; Pred. No. 1.3e-24;
Matches 53; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 GPGTKKVHVFYKGNLKNKDIRCKDDYTHLYTLIVRPDNTYEVKIDNKVSGSLE 60
|||||
Db 133 GPGTKKVHVFYKGNLKNKDIRCKDDSFTHLYTLIVRPDNTYEVKIDNKVSGSLE 192
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RESULT 5
Q72WU8 PRELIMINARY; PRT; 413 AA.
ID Q72WU8
AC Q72WU8;
DT 01-JUN-2003 (TREMBlrel. 24, Created)

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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to calreticulin.
OC Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC046699; AAH46699.1; -
GO; GO:0005514; F:calcium ion storage activity; IEA.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR009033; Calret calnex P.
DR InterPro; IPR008985; ConA like lec_gl.
DR InterPro; IPR000886; ER target S.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
DR PROSITE; PS00014; ER TARGET; 1.
SQ SEQUENCE 413 AA; 48521 MW; DE002F8F0523772B CRC64;

Query Match 87.4%; Score 278; DB 13; Length 413;
Best Local Similarity 88.3%; Pred. No. 1.3e-24;
Matches 53; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GPGTKKHVHVIENYKGNVLINCKDDEFTHTLTVLRPDNTYEVKIDNSQVESGSL 60
Db 139 GPPTKKHVHVIENYKGNVLINCKDDEFTHTLTVLRPDNTYEVKIDNSQVESGSL 198

RESULT 6
Q7ZXY3
ID Q7ZXY3 PRELIMINARY; PRT; 418 AA.
AC Q7ZXY3;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to calreticulin.
OC Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC044069; AAH44069.1; -
GO; GO:0005514; F:calcium ion storage activity; IEA.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR009033; Calret calnex P.
DR InterPro; IPR008985; ConA like lec_gl.
DR InterPro; IPR000886; ER target S.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 2.
DR PROSITE; PS00014; ER TARGET; 1.
SQ SEQUENCE 418 AA; 49028 MW; 731C1C9AA08F9A53 CRC64;

Query Match 87.4%; Score 278; DB 13; Length 418;
Best Local Similarity 88.3%; Pred. No. 1.3e-24;
Matches 53; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

1 GPGTKKHVHVIENYKGNVLINCKDDEFTHTLTVLRPDNTYEVKIDNSQVESGSL 60
139 GPPTKKHVHVIENYKGNVLINCKDDEFTHTLTVLRPDNTYEVKIDNSQVESGSL 198

RESULT 7
Q8IS63
ID Q8IS63 PRELIMINARY; PRT; 403 AA.
AC Q8IS63;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Calreticulin.
OC Cotesia rubecula.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Ichneumonicoidea;
OC Braconidae; Microgasterinae; Cotesia.
OX NCBI_TaxID=32392;
RN [1]
RP SEQUENCE FROM N.A.
RA Asgari S., Zhang G., Schmidt O.;
RT "polydnavirus particle proteins with similarities to molecular
chaperons, heat shock protein 70 and calreticulin."
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF150370; AAN73309.1; -
GO; GO:0005514; F:calcium ion storage activity; IEA.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR009033; Calret calnex P.
DR InterPro; IPR008985; ConA like lec_gl.
DR InterPro; IPR000886; ER target S.
DR Pfam; PF00262; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 2.
DR PROSITE; PS00014; ER TARGET; 1.
SQ SEQUENCE 403 AA; 46550 MW; 259D771A822DB126 CRC64;

Query Match 86.8%; Score 276; DB 5; Length 403;
Best Local Similarity 83.3%; Pred. No. 2.2e-24;
Matches 50; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GPGTKKHVHVIENYKGNVLINCKDDEFTHTLTVLRPDNTYEVKIDNSQVESGSL 60
Db 137 GPGTKKHVHVIENYKGNVLINCKDDEFTHTLTVLRPDNTYEVKIDNSQVESGSL 196

RESULT 8
Q86G72
ID Q86G72 PRELIMINARY; PRT; 407 AA.
AC Q86G72;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Calreticulin.
OC Dermacentor variabilis.
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Parasitiformes; Ixodida; Ixodidae; Dermacentor.
OX NCBI_TaxID=34621;
RN [1]
RP SEQUENCE FROM N.A.
RA Simser J.A., Muelenga A., Macaluso K.R., Azad A.F.;
RT "Molecular characterization of Dermacentor variabilis calreticulin."
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY241957; AAC92278.1; -
GO; GO:0005514; F:calcium ion storage activity; IEA.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR009033; Calret calnex P.
DR InterPro; IPR008985; ConA like lec_gl.
DR InterPro; IPR000886; ER target S.
DR Pfam; PF00262; calreticulin; 1.
SQ SEQUENCE 407 AA; 46550 MW; 259D771A822DB126 CRC64;

RN		SEQUENCE FROM N.A.	
RP	Susan J.M., Just M.L., Lennarz W.J.;		
RA	"Cloning and Characterization of Alpha Integrin and Calreticulin in		
RT	Embryos of the Sea Urchin."		
RL	Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.		
EL	Submited (AUG-1999) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF17915; AAD55725.1; -		
DR	GO; GO:0005514; F:calcium ion storage activity; IEA.		
DR	InterPro; IPR001580; Calreticulin.		
DR	InterPro; IPR009033; Calret calnex P.		
DR	InterPro; IPR008985; ConA like lec_gl.		
DR	InterPro; IPR000886; ER target_S.		
DR	Pfam; PF00262; calreticulin; 1.		
DR	PRINTS; PS00626; CALRETICULIN.		
DR	ProDom; PD001866; Calreticulin; 1.		
DR	PROSITE; PS00804; CALRETICULIN 2; 1.		
DR	PROSITE; PS00805; CALRETICULIN REPEAT; 3.		
DR	PROSITE; PS00014; ER_TARGET; 1.		
KW	Signal.		
FT	SIGNAL	1 19 POTENTIAL.	
FT	CHAIN	20 421 CALRETICULIN.	
SQ	SEQUENCE	421 AA; 48822 MW; 172C664F59F41F93 CRC64;	
	Query Match	84.9%; Score 270; DB 5; Length 421;	
	Best Local Similarity	80.0%; Pred.No. 1.2e-23;	
	Matches	48; Conservative	8; Mismatches 4; Indels 0; Gaps 0;
QY	1	GPGTKKVHVIIFYNGKGVNLINKDIRCKDDFFTHLYTLIVRDPNTYEVKIDNSQVESGSL	60
Db	137	GPGTKKVHVIIFYNGKGVNLINKDIRCKDDFFTHLYTLIVRDPNTYEVKIDNSQVESGSL	196
RESULT	11		
Q9U916		PRELIMINARY; PR7; 406 AA.	
ID	Q9U916		
AC	Q9U916;		
DT	01-MAY-2000 (TREMBLrel. 13, Created)		
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)		
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)		
DE	Calreticulin.		
DE	Calreticulin.		
CNC	OR CG9429.		
GN	Drosophila melanogaster (Fruit fly).		
OS	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;		
OC	Nectera; Endopterygota; Diptera; Brachycera; Muscomorpha;		
OC	Ephydroidea; Drosophilidae; Drosophila.		
OX	NCBI_Taxid=7227;		
[1]	_Taxid=7227;		
PP	SEQUENCE FROM N.A.		
RC	STRAIN=CRCO-N-R;		
RA	Dodo K., Sakoyama Y., Gamo S.;		
RL	"Drosophila melanogaster calreticulin for mRNA";		
RT	Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AB000718; BAA85379.1; -		
DR	FlyBase; FBgn0005585; Crc.		
DR	GO; GO:0007417; P:central nervous system development; IMP.		
DR	InterPro; IPR001580; Calreticulin.		
DR	InterPro; IPR009033; Calret calnex P.		
DR	InterPro; IPR008985; ConA like lec_gl.		
DR	InterPro; IPR000886; ER target_S.		
DR	Pfam; PF00262; calreticulin; 1.		
DR	PRINTS; PS00626; CALRETICULIN.		
DR	ProDom; PD001866; Calreticulin; 1.		
DR	PROSITE; PS00803; CALRETICULIN 1; 1.		
DR	PROSITE; PS00804; CALRETICULIN 2; 1.		
DR	PROSITE; PS00805; CALRETICULIN REPEAT; 3.		
DR	PROSITE; PS00014; ER_TARGET; 1.		
SQ	SEQUENCE	406 AA; 46809 MW; 68BA49A6B81CC427 CRC64;	
	Query Match	84.6%; Score 269; DB 5; Length 406;	
	Best Local Similarity	83.3%; Pred.No. 1.5e-23;	
	Matches	50; Conservative	5; Mismatches 5; Indels 0; Gaps 0;
OY	1	GPGTKKVHVIIFYNGKGVNLINKDIRCKDDFFTHLYTLIVRDPNTYEVKIDNSQVESGSL	60

1 GPGTKKVVHVFYFNKGKNVLINRCKDDDEFTHLYLVIRPDPNTYEVDKINSQVSGSLG 60
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 138 GPGTKKVVHVFYFNKGKNHLIKRCKDDVYTHLYTLVKPDNTYEVLIDNEKVESGGLE 197

RESULT 14

QSWPG8	PRELIMINARY;	PRT; 397 AA.
ID Q8NPG8		
AC Q8NPG8;		
DT 01-MAR-2002 (TrEMBLrel. 20, Created)		
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)		
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)		
DE Calreticulin.		
OS Galleria mellonella (Wax moth).		
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;		
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Pyraloidea;		
OC Pyralidae; Galleriinae; Galleria.		
OX NCBI_TaxID=7137;		
RN [1]		
RC TISSUE=FROM N.A.		
RP TISSUE=Larva;		
RA Choi J.Y., Whitten M.A., Cho M.Y., Lee K.Y., Kim M.S., Ratcliffe N.,		
RA Lee B.L.;		
RT "Calreticulin enriched as an early-staged encapsulation protein in wax		
RT moth <i>Galleria mellonella</i> larvae;purification and molecular cloning.";		
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.		
DR EMBL; AB063250; BAB79277.1; -.		
DR GO; GO:0005514; F:calcium ion storage activity; IEA.		
DR InterPro; IPR001580; Calreticulin.		
DR InterPro; IPR009033; Calret calnex P.		
DR InterPro; IPR008985; ConA like lec_gl.		
DR InterPro; IPR000886; ER_target_S.		
DR Pfam; PF00262; calreticulin; 1.		
DR PRINTS; P00626; CALRETICULIN.		
DR ProDom; PD001866; Calreticulin; 1.		
DR PROSITE; PS00803; CALRETICULIN 1; 1.		
DR PROSITE; PS00804; CALRETICULIN 2; 1.		
DR PROSITE; PS00805; CALRETICULIN REPEAT; 3.		
DR PROSITE; PS00014; ER_TARGET_1.		
SQ SEQUENCE 397 AA; 46024 MW; 211235D6950657F4 CRC64;		

Query Match 84.0%; Score 267; DS 5; Length 397;
 Best Local Similarity 81.7%; Pred.No.2.5e-23;
 Matches 49; Conservative 5; Mismatches 0; Gaps 60

QY 1 GPGTKKVVHVFYFNKGKNVLINRCKDDDEFTHLYLVIRPDPNTYEVDKINSQVSGSLG 60
 :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 138 GPGTKKVVHVFYFNKGKNHLIKRCKDDVYTHLYTLVKPDNTYEVLIDNEKVESGGLE 197

[illegible]

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276		139

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RESULT 13
Q7Z1E6 PRELIMINARY; PRT; 398 AA.
ID Q7Z1E6 AC Q7Z1E6
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Calreticulin.
OS Bombyx mori (silkworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Bombycoidea;
OC Bombycidae; Bombyx.
NCBI_TaxID=7091;
RN [1]
RP SEQUENCE FROM N.A.
RA Kim S.R., Lee K.S., Kim I., Kang S.W., Kho S.K., Sohn H.D., Jin B.R.;
RT "Molecular cloning of a cDNA encoding putative calreticulin from the
RT silkworm, Bombyx mori."
RL Int. J. Indust. Entomol. 6:93-97(2003).
DR EMBL; AY297158; AAP50845.1; -.
SQ SEQUENCE 398 AA; 45801 MW; 0BC049839F5950EA CRC64;
Query Match 84.3%; Score 268; DB 5; Length 398;
Best Local Similarity 83.3%; Pred. No. 1,9e-23;
Accession: AY297158; Accession: AAP50845.1; Models: 0; Gaps: 5;

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RP SEQUENCE FROM N.A.
 RC TISSUE=Salivary gland;
 RA Jaworski D.C.;
 RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Salivary gland;
 RA Fain-Thornton J.M., Jaworski D.C., Needham G.R.;
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U07708; AAC79094.1; -;
 DR GO; GO:0005514; F:calcium ion storage activity; IEA.
 DR InterPro; IPR001580; Calreticulin.
 DR InterPro; IPR009033; Calret_calmex_P.
 DR InterPro; IPR008985; ConA_like lec_gl.
 DR InterPro; IPR000886; ER_target_S.
 DR Pfam; PF00262; calreticulin; 1.
 DR PRINTS; PR00626; CALRETICULIN.
 DR ProDom; PD001866; Calreticulin; 1.
 DR PROSITE; PS00803; CALRETICULIN_1; 1.
 DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
 DR PROSITE; PS00014; ER_TARGET; 1.
 SQ SEQUENCE 410 AA; 47485 MW; 32CCB8750A17DC54 CRC64;

Query Match 84.0%; Score 267; DB 5; Length 410;
 Best Local Similarity 83.3%; Pred. No. 2.6e-23;
 Matches 50; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
 Qy 1 GPCTKKVHVFYKGNVLINKDIRCKDBEFTHLYTLIVRPDNTVEVKIDNSQVESGSLE 60
 Db 137 GPCTKKVHVFYKGNVHLINKDIRCKDDVFTHLYTLIVKPDNTYVWKIDNEVAKGELE 196

Search completed: October 4, 2004, 13:05:52
 Job time : 36.3529 secs

OM protein - protein search, using sw model

Run on: October 4, 2004, 12:50:22 ; Search time 45.5294 Seconds
(without alignments)
372.349 Million cell updates/sec

Title: US-09-807-148-8

Perfect score: 318

Sequence: 1 GGTGKKVHFVFNKGNVLI.....PDNTYEVKIDNSQVESGSL 60

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_28Jan04: *
1: geneseqp1980s: *
2: geneseqp1990s: *
3: geneseqp2000s: *
4: geneseqp2001s: *
5: geneseqp2002s: *
6: geneseqp2003as: *
7: geneseqp2003bs: *
8: geneseqp2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	318	100.0	60	3	AAY92354 Recombina
2	318	100.0	61	3	AAY92352 Recombina
3	318	100.0	180	3	AAY92351 Human vas
4	318	100.0	280	3	AAY92355 Recombina
5	318	100.0	400	3	AAY92350 Recombina
6	318	100.0	401	2	AAY11156 Calreticu
7	318	100.0	416	7	AD56306 Rat Prote
8	318	100.0	416	7	AD56310 Rat Prote
9	318	100.0	417	1	AAP92276 60 kD Ro
10	318	100.0	417	2	AAY00927 Calreticu
11	318	100.0	417	3	AAY92349 Human MBP
12	318	100.0	417	5	AAY7712 Human cal
13	318	100.0	417	5	AAY24591 Human cal
14	318	100.0	417	5	AAE18851 Human cal
15	318	100.0	417	5	AB382384 Human cal
16	318	100.0	417	6	ABJ19766 Human MP2
17	318	100.0	417	6	AG79824 Calreticu
18	318	100.0	417	6	ADA26337 Human cal
19	318	100.0	417	7	AD22407 HLA-B46 T
20	318	100.0	417	7	AD56308 Human Pro
21	318	100.0	417	7	AD56312 Human Pro
22	272	85.5	403	2	AAW04171 Flea calr
23	269	84.6	406	4	AB64414 Drosophil
24	258	81.1	49	3	AAY92353 Recombina
25	242	76.1	336	2	AAI2312 Partial s

26	190	59.7	122	2	AAY00926 Rat CCLQR
27	190	59.7	122	2	AAY00924 Human CCL
28	182	57.2	122	2	AAY00925 Mouse cC1
29	177	55.7	415	4	AA66343 Castor be
30	177	55.7	415	4	AA66341 Castor be
31	176	55.3	419	7	ABW74155 DNA clone
32	175	55.0	385	3	AB332385 Human sec
33	175	55.0	390	6	ABO07134 Novel hum
34	171	53.8	428	7	ABW74288 DNA clone
35	170	53.5	420	5	ABW04856 Maize cal
36	169	53.1	312	3	AA647933 Arabidops
37	169	53.1	312	3	AA624609 Arabidops
38	169	53.1	332	3	AA630998 Arabidops
39	169	53.1	421	3	AA624608 Arabidops
40	169	53.1	421	3	AA647932 Arabidops
41	169	53.1	424	3	AA624607 Arabidops
42	169	53.1	424	3	AA647931 Arabidops
43	169	53.1	441	3	AA630997 Arabidops
44	169	53.1	444	3	AA630996 Arabidops
45	117	36.8	592	4	ABB44554 Human wou

ALIGNMENTS

RESULT 1

AA92354
ID AAY92354 standard; protein; 60 AA.

XX
AC AAY92354;

XX
DT 10-AUG-2000 (first entry)

XX
DE Recombinant human calreticulin residues 121-180.

XX
KW MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;
XX
KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
XX
KW cytosolic; dermal; immunosuppressive; anti-inflammatory; hepatic;
XX
KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.

OS Homo sapiens.

OS Synthetic.

XX
PN WO200020577-A1.

XX
PD 13-APR-2000.

XX
PF 05-OCT-1999; 99WO-US023240.

XX
PR 06-OCT-1998; 98US-0103438P.

XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX
PI Tosato G, Pike SE, Yao L;

XX
DR WPI; 2000-303767/26.

XX
PT Inhibiting endothelial cell growth and angiogenesis using calreticulin,

XX
PS useful for suppressing tumor growth.

XX
PP Claim 4; Page 85; 99pp; English.

XX
CC A novel method of inhibiting endothelial cell growth comprises contacting
XX
CC the cells with calreticulin (or its fragments/variants). Fragments of
XX
CC calreticulin causes at least 40% inhibition of angiogenesis, tumor growth
XX
CC and/or endothelial cell growth (claimed). The method may be used for
XX
CC inhibiting angiogenesis in a patient. The angiogenesis is associated with
XX
CC a disease other than a tumor that is associated with neovascularization
XX
CC (e.g. diabetic neuropathy, retrolental fibroplasia, trachoma, neovascular
XX
CC glaucoma, psoriasis, angiofibromas, immune inflammation,
XX
CC atherosclerosis, excessive wound repair, retinal neovascularization,
XX
CC macular degeneration, corneal graft rejection, contact lens overwear,
XX
CC Crohn's disease, non-immune inflammation, rheumatoid arthritis, systemic

CC lupus erythematosus, thyroiditis, Goodpasture's syndrome, systemic
 CC vasculitis, scleroderma, Sjorgen's syndrome, sarcoidosis and primary
 CC biliary cirrhosis). The method may also be used for treating/inhibiting
 CC tumor growth especially Kaposi's sarcoma (claimed)

XX Sequence 60 AA;

Query Match 100.0%; Score 318; DB 3; Length 60;
 Best Local Similarity 100.0%; Pred. No. 3e-37;
 Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPQTKKVHVFNYKGNVLINKDIRCKDDEFTHLYTLVLRPNTYEVKIDNSQVSGSLE 60
 |||||
 Db 1 GPQTKKVHVFNYKGNVLINKDIRCKDDEFTHLYTLVLRPNTYEVKIDNSQVSGSLE 60

RESULT 2

AA92352
 ID AAY92352 standard; protein; 61 AA.

XX
 AC AAY92352;

XX
 DT 10-AUG-2000 (first entry)

XX
 DE Recombinant human calreticulin residues 120-180.

XX MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;
 KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
 KW cytotactic; dermalogical; immunosuppressive; antiinflammatory; hepatic;
 KW anti-atherosclerotic; Gastrointestinal; anti-arthritis; ophthalmic.

XX Homo sapiens.

OS Synthetic.

XX WO200020577-A1.

PN 13-APR-2000.

PD 05-OCT-1999; 99WO-US023240.

PF 06-OCT-1998; 98US-0103438P.

PR (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Tosato G, Pike SE, Yao L;

XX WPI; 2000-303767/26.

XX Inhibiting endothelial cell growth and angiogenesis using calreticulin,
 PT useful for suppressing tumor growth.

XX Claim 4; Page 82-83; 99pp; English.

XX A novel method of inhibiting endothelial cell growth comprises contacting
 CC the cells with calreticulin (or its fragments/variants). Fragments of
 CC calreticulin causes at least 40% inhibition of angiogenesis, tumor growth
 CC and/or endothelial cell growth (claimed). The method may be used for
 CC inhibiting angiogenesis in a patient. The angiogenesis is associated with
 CC a disease other than a tumor that is associated with neovascularization
 CC (e.g. diabetic neuropathy, retrolental fibroplasia, trachoma, neovascular
 CC glaucoma, psoriasis, angiofibromas, immune inflammation,
 CC atherosclerosis, excessive wound repair, retinal neovascularization,
 CC macular degeneration, corneal graft rejection, contact lens overwear,
 CC Crohn's disease, non-immune inflammation, rheumatoid arthritis, systemic
 CC lupus erythematosus, thyroiditis, Goodpasture's syndrome, systemic
 CC vasculitis, scleroderma, Sjorgen's syndrome, sarcoidosis and primary
 CC biliary cirrhosis). The method may also be used for treating/inhibiting
 CC tumor growth especially Kaposi's sarcoma (claimed)

XX Sequence 61 AA;

Query Match 100.0%; Score 318; DB 3; Length 61;
 Best Local Similarity 100.0%; Pred. No. 3.1e-37;

Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GPQTKKVHVFNYKGNVLINKDIRCKDDEFTHLYTLVLRPNTYEVKIDNSQVSGSLE 60
 |||||
 Db 2 GPQTKKVHVFNYKGNVLINKDIRCKDDEFTHLYTLVLRPNTYEVKIDNSQVSGSLE 61

RESULT 3

AA92351
 ID AAY92351 standard; protein; 180 AA.

XX
 AC AAY92351;

XX
 DT 10-AUG-2000 (first entry)

XX Human vasostatin (calreticulin N-terminal 180 amino acids).

XX MBP-calreticulin; maltose binding protein; vasostatin; N-terminal;
 KW angiogenesis; inhibition; endothelial cell; anti-angiogenic;
 KW neuroprotective; antidiabetic; cytostatic; dermalogical; hepatic;
 KW immunosuppressive; antiinflammatory; anti-atherosclerotic;
 KW gastrointestinal; anti-arthritis; ophthalmic.

XX Homo sapiens.

OS Synthetic.

XX WO200020577-A1.

PN 13-APR-2000.

PD 05-OCT-1999; 99WO-US023240.

PF 06-OCT-1998; 98US-0103438P.

PR (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Tosato G, Pike SE, Yao L;

XX WPI; 2000-303767/26.

XX Inhibiting endothelial cell growth and angiogenesis using calreticulin,
 PT useful for suppressing tumor growth.

XX Claim 4; Page 82; 99pp; English.

XX A novel method of inhibiting endothelial cell growth comprises contacting
 CC the cells with calreticulin (or its fragments/variants). Fragments of
 CC calreticulin causes at least 40% inhibition of angiogenesis, tumor growth
 CC and/or endothelial cell growth (claimed). The method may be used for
 CC inhibiting angiogenesis in a patient. The angiogenesis is associated with
 CC a disease other than a tumor that is associated with neovascularization
 CC (e.g. diabetic neuropathy, retrolental fibroplasia, trachoma, neovascular
 CC glaucoma, psoriasis, angiofibromas, immune inflammation,
 CC atherosclerosis, excessive wound repair, retinal neovascularization,
 CC macular degeneration, corneal graft rejection, contact lens overwear,
 CC Crohn's disease, non-immune inflammation, rheumatoid arthritis, systemic
 CC lupus erythematosus, thyroiditis, Goodpasture's syndrome, systemic
 CC vasculitis, scleroderma, Sjorgen's syndrome, sarcoidosis and primary
 CC biliary cirrhosis). The method may also be used for treating/inhibiting
 CC tumor growth especially Kaposi's sarcoma (claimed)

XX Sequence 180 AA;

Query Match 100.0%; Score 318; DB 3; Length 180;
 Best Local Similarity 100.0%; Pred. No. 1.2e-36;
 Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPQTKKVHVFNYKGNVLINKDIRCKDDEFTHLYTLVLRPNTYEVKIDNSQVSGSLE 60
 |||||
 Db 121 GPQTKKVHVFNYKGNVLINKDIRCKDDEFTHLYTLVLRPNTYEVKIDNSQVSGSLE 180

RESULT 4

```

AA92355
ID AAY92355 standard; protein; 280 AA.
XX
AC AAY92355;
XX
XX 10-AUG-2000 (first entry)
DT
DE Recombinant delta-120 calreticulin.
XX
XX MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;
KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
KW cytosolic; dermatological; immunosuppressive; anti-inflammatory; hepatic;
KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.
XX
OS Homo sapiens.
XX
XX WO200020577-A1.
XX
XX 13-APR-2000.
XX
XX MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;
KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
KW cytosolic; dermatological; immunosuppressive; anti-inflammatory; hepatic;
KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX WO200020577-A1.
XX
XX 13-APR-2000.
XX
XX 05-OCT-1999; 99WO-US023240.
XX
XX 06-OCT-1998; 98US-0103438P.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Tosato G, Pike SE, Yao L;
XX
XX WPI; 2000-303767/26.
XX
XX Inhibiting endothelial cell growth and angiogenesis using calreticulin,
PT useful for suppressing tumor growth.
XX
XX Claim 4; Page 86; 99pp; English.
XX
XX This sequence comprises recombinant human calreticulin (AA92350) missing
CC the N-terminal 120 amino acids. A novel method of inhibiting endothelial
CC cell growth comprises contacting the cells with calreticulin (or its
CC fragments/variants). Fragments of calreticulin causes at least 40%
CC inhibition of angiogenesis, tumor growth and/or endothelial cell growth
CC (claimed). The method may be used for inhibiting angiogenesis in a
CC patient. The angiogenesis is associated with a disease other than a tumor
CC that is associated with neovascularization (e.g. diabetic neuropathy,
CC retrolental fibroplasia, trachoma, neovascular glaucoma, psoriasis,
CC angiofibromas, immune inflammation, atherosclerosis, excessive wound
CC repair, retinal neovascularization, macular degeneration, corneal graft
CC rejection, contact lens overwear, Crohn's disease, non-immune
CC inflammation, rheumatoid arthritis, systemic lupus erythematosus,
CC thyroiditis, Goodpasture's syndrome, systemic vasculitis, scleroderma,
CC Sjorgen's syndrome, sarcoidosis and primary biliary cirrhosis). The
CC method may also be used for treating/inhibiting tumor growth especially
CC Kaposi's sarcoma (claimed)
XX
XX Sequence 280 AA;
SQ
Query Match 100.0%; Score 318; DB 3; Length 280;
Best Local Similarity 100.0%; Pred. No. 2.2e-36;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPGTKKHVIFNYKGNVLINKDKDDEFTHTLTVLRPDNTYEVKIDNSQVSGSLE 60
DB 1 GPGTKKHVIFNYKGNVLINKDKDDEFTHTLTVLRPDNTYEVKIDNSQVSGSLE 60

RESULT 5
RAY92350
ID AAY92350 standard; protein; 400 AA.
XX
AC AAY92350;
XX
XX 10-AUG-2000 (first entry)
DT
DE Recombinant human MBP-calreticulin.
XX
XX MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;
KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
KW cytosolic; dermatological; immunosuppressive; anti-inflammatory; hepatic;
KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.
XX
OS Homo sapiens.
XX
XX WO200020577-A1.
XX
XX 13-APR-2000.
XX
XX MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;
KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
KW cytosolic; dermatological; immunosuppressive; anti-inflammatory; hepatic;
KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.
XX
OS Homo sapiens.
XX
XX WO200020577-A1.
XX
XX 13-APR-2000.
XX
XX 05-OCT-1999; 99WO-US023240.
XX
XX 06-OCT-1998; 98US-0103438P.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Tosato G, Pike SE, Yao L;
XX
XX WPI; 2000-303767/26.
XX
XX Inhibiting endothelial cell growth and angiogenesis using calreticulin,
PT useful for suppressing tumor growth.
XX
XX Claim 4; Page 80-81; 99pp; English.
XX
XX Recombinant human MBP-calreticulin comprises the sequence of human
CC calreticulin (see AA92349) without the 17 N-terminal amino acids. A
CC novel method of inhibiting endothelial cell growth comprises contacting
CC the cells with calreticulin (or its fragments/variants). Fragments of
CC calreticulin causes at least 40% inhibition of angiogenesis, tumor growth
CC and/or endothelial cell growth (claimed). The method may be used for
CC inhibiting angiogenesis in a patient. The angiogenesis is associated with
CC a disease other than a tumor that is associated with neovascularization
CC (e.g. diabetic neuropathy, retrolental fibroplasia, trachoma, neovascular
CC glaucoma, psoriasis, angiofibromas, immune inflammation,
CC atherosclerosis, excessive wound repair, retinal neovascularization,
CC macular degeneration, corneal graft rejection, contact lens overwear,
CC Crohn's disease, non-immune inflammation, rheumatoid arthritis, systemic
CC lupus erythematosus, thyroiditis, Goodpasture's syndrome, sarcoidosis and primary
CC biliary cirrhosis). The method may also be used for treating/inhibiting
CC tumor growth especially Kaposi's sarcoma (claimed)
XX
XX Sequence 400 AA;
SQ
Query Match 100.0%; Score 318; DB 3; Length 400;
Best Local Similarity 100.0%; Pred. No. 3.5e-36;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPGTKKHVIFNYKGNVLINKDKDDEFTHTLTVLRPDNTYEVKIDNSQVSGSLE 60
DB 121 GPGTKKHVIFNYKGNVLINKDKDDEFTHTLTVLRPDNTYEVKIDNSQVSGSLE 180

RESULT 6
AAW11156
ID AAW11156 standard; peptide; 401 AA.
XX
AC AAW11156;
XX
XX 31-MAY-1997 (first entry)
DT
DE Calreticulin.
XX
KW calreticulin; C-domain; restenosis; inhibitor.
XX
OS Homo sapiens.
XX
XX WO9636643-A1.
XX
XX

```

XX 21-NOV-1996.
 XX PD
 XX PF
 XX PF 17-MAY-1996; 96WO-IB000471.
 XX
 XX PR 17-MAY-1995; 95US-00442844.
 XX PR 16-MAY-1996; 96US-00649417.
 XX
 XX PA (UYAL-) UNIV ALBERTA.
 XX
 XX PI Michalak M, Lucas A;
 XX
 XX DR WPI; 1997-012036/01.
 XX
 XX FT Inhibition of restenosis in patients - using calreticulin or a C-domain
 XX FT polypeptide of calreticulin or a variant with the same activity.
 XX PS Disclosure; Fig 1; 48pp; English.
 XX
 XX CC The present sequence is calreticulin. It and a C-domain derived peptide
 XX CC (AAW06736) are useful for treating a patient to inhibit restenosis. The
 XX CC calreticulin-type cpds. are administered either parenterally,
 XX CC intravenously or via a catheter and can target areas of vascular damage
 XX CC to inhibit or prevent restenosis
 XX
 XX SQ Sequence 401 AA;
 XX
 XX Query Match 100.0%; Score 318; DB 2; Length 401;
 XX Best Local Similarity 100.0%; Pred. No. 3.5e-36;
 XX Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1 GPGTKVHVIFNFKGNVLINKDIRCKDDEFTHLVTLVLRPNTVEVKIDNSQVSGSLE 60
 XX Db 121 GPGTKVHVIFNFKGNVLINKDIRCKDDEFTHLVTLVLRPNTVEVKIDNSQVSGSLE 180
 XX
 XX RESULT 7
 XX ADE56306
 XX ID ADE56306 standard; protein; 416 AA.
 XX AC ADE56306;
 XX
 XX DT 29-JAN-2004 (first entry)
 XX
 XX DE Rat Protein P18418, SEQ ID NO 2158.
 XX
 XX KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
 XX KW Chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
 XX
 XX OS Rattus norvegicus.
 XX
 XX PN WO2003016475-A2.
 XX
 XX PD 27-FEB-2003.
 XX
 XX PF 14-AUG-2002; 2002WO-US025765.
 XX
 XX PR 14-AUG-2001; 2001US-0312147P.
 XX PR 01-NOV-2001; 2001US-0346382P.
 XX PR 26-NOV-2001; 2001US-0333347P.
 XX
 XX PA (GCHO) GEN HOSPITAL CORP.
 XX PA (FARB) BAYER AG.
 XX
 XX PI Woolf C, D'urso D, Befort K, Costigan M;
 XX
 XX DR WPI; 2003-268312/26.
 XX DR GENBANK; P18418.
 XX
 XX FT New composition comprising two or more isolated polypeptides, useful for
 XX FT preparing a medicament for treating pain in an animal.
 XX
 XX PS Claim 1; Page; 1017pp; English.

XX
 CC The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 XX SQ Sequence 416 AA;
 XX
 XX Query Match 100.0%; Score 318; DB 7; Length 416;
 XX Best Local Similarity 100.0%; Pred. No. 3.7e-36;
 XX Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1 GPGTKVHVIFNFKGNVLINKDIRCKDDEFTHLVTLVLRPNTVEVKIDNSQVSGSLE 60
 XX Db 138 GPGTKVHVIFNFKGNVLINKDIRCKDDEFTHLVTLVLRPNTVEVKIDNSQVSGSLE 197
 XX
 XX RESULT 8
 XX ADE56310
 XX ID ADE56310 standard; protein; 416 AA.
 XX AC ADE56310;
 XX
 XX DT 29-JAN-2004 (first entry)
 XX
 XX DE Rat Protein P18418, SEQ ID NO 2162.
 XX
 XX KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
 XX KW Chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
 XX
 XX OS Rattus norvegicus.
 XX
 XX PN WO2003016475-A2.
 XX
 XX PD 27-FEB-2003.
 XX
 XX PF 14-AUG-2002; 2002WO-US025765.
 XX
 XX PR 14-AUG-2001; 2001US-0312147P.
 XX PR 01-NOV-2001; 2001US-0346382P.
 XX PR 26-NOV-2001; 2001US-0333347P.
 XX
 XX PA (GCHO) GEN HOSPITAL CORP.
 XX PA (FARB) BAYER AG.
 XX
 XX PI Woolf C, D'urso D, Befort K, Costigan M;
 XX
 XX DR WPI; 2003-268312/26.
 XX DR GENBANK; P18418.
 XX
 XX FT New composition comprising two or more isolated polypeptides, useful for
 XX FT preparing a medicament for treating pain in an animal.
 XX
 XX PS Claim 1; Page; 1017pp; English.

PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 416 AA;

Query Match 100.0%; Score 318; DB 7; Length 416;
Best Local Similarity 100.0%; Pred. No. 3.7e-36;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPGTKKVHVIFNYGKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSL 60
Db 138 GPGTKKVHVIFNYGKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSL 197

RESULT 9
AAP92276
ID AAP92276 standard; protein; 417 AA.
XX
XX AAP92276;
XX
XX 25-MAR-2003 (revised)
XX 23-FEB-1990 (first entry)
XX
XX 60 kD Ro (Ro/SSA) antigen.
XX
XX Sjorens syndrome; systemic lupus erythematosus.
XX Synthetic.
XX WO8909273-A.
XX
XX 05-OCT-1989.
XX
XX 22-MAR-1989; 89WO-US001213.
XX
XX 22-MAR-1988; 88US-00171634.
XX (TEXA) UNIV TEXAS SYSTEM.
XX
XX Sontheimer RD, Lieu TS, Capra JD, Mccaulliffe DP;
XX WPI; 1989-309537/42.
XX N-PSDB; AAP92276.
XX

XX DNA sequences encoding antigenic epitope(s) of RO 60 KD auto-antigen -
PT used in immunoassays to detect rheumatic disease.
XX
XX Disclosure; Fig 2; 88pp; English.
XX
XX Synthetic peptides corresp. to an epitopic core of Ro antigen are
CC expressed recombinantly to detect autoantibodies, for identification of
CC autoimmune diseases. These epitopes are AAs 24-36, 23-36, 188-209, or 241
CC -255. The peptides may be substd. for ribonucleoprotein particle
CC antigens. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-
CC MAR-2003 to correct PI field.)
XX
XX Sequence 417 AA;

Query Match 100.0%; Score 318; DB 1; Length 417;
Best Local Similarity 100.0%; Pred. No. 3.7e-36;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPGTKKVHVIFNYGKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSL 60
Db 138 GPGTKKVHVIFNYGKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSL 197

RESULT 10
AAY00927
ID AAY00927 standard; protein; 417 AA.
XX
XX AAY00927;
XX
XX 28-MAY-1999 (first entry)
XX
XX Calreticulin.
XX
XX C1g and collectin receptor; cClqR binding domain; complement ubiquitin;
KW C1g and collectin receptor; inhibitor; complement activation; inflammation;
KW myocardial infarction; brain ischaemia; gut ischaemia; amyloid plaque;
KW rheumatoid arthritis; systemic lupus erythematosus; Alzheimer's disease;
KW immune complex nephritis; therapy.
XX
XX Homo sapiens.
XX WO9507406-A1.
XX
XX 18-FEB-1999.
XX
XX 12-AUG-1998; 98WO-GB002430.
XX
XX 12-AUG-1997; 97GB-00016998.
XX (UYLE-) UNIV LEICESTER.
XX
XX Schwaebler W;
XX
XX WPI; 1999-180404/15.
XX
XX Use of a cClqR binding domain - to modulate complement ubiquitin (CUB)
PT functionality.
XX
XX Disclosure; Page 26-27; 31pp; English.
XX
XX This sequence is calreticulin, a homologue of C1g and collectin receptor
CC (cClqR). The invention relates to the use of a cClqR binding domain in a
CC medicament to effect complement ubiquitin (CUB) functionality, and an
CC inhibitor of the cClqR binding domain in a medicament to inhibit CUB
CC functionality. The cClqR binding domain, or its inhibitor, can be used to
CC treat a human or animal body. Particularly an inhibitor is used to treat
CC complement activation involved in the initiation and maintenance of
CC inflammation, for example in myocardial infarction, brain ischaemia
CC (stroke), gut ischaemia, rheumatoid arthritis, systemic lupus
CC erythematosus, burns, immune complex nephritis, and to treat amyloid
CC plaques in Alzheimer's disease. The use of cClqR binding domain or
CC inhibitor enables the CUB domain functionality to be modulated using a

CC low molecular weight molecule
 XX Sequence 417 AA;
 SQ

Query Match 100.0%; Score 318; DB 2; Length 417;
 Best Local Similarity 100.0%; Pred. No. 3.7e-36;
 Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPGTKVHVIFNYKGNVLINKDIRCKDDEFTHLTYLIVRPDNTYEVKIDNSQVSGSLE 60
 |||||
 Db 138 GPGTKVHVIFNYKGNVLINKDIRCKDDEFTHLTYLIVRPDNTYEVKIDNSQVSGSLE 197

RESULT 11
 AAY92349
 ID AAY92349 standard; protein; 417 AA.
 XX
 AC AAY92349;
 XX
 DT 10-AUG-2000 (first entry)
 XX
 DE Human MBP-calreticulin.
 XX
 KW MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;
 endotheial cell; anti-angiogenic; neuroprotective; antidiabetic;
 KW cytostatic; dermatological; immunosuppressive; antiinflammatory; hepatic;
 anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FT Peptide 1..17 Location/Qualifiers
 FT Protein 18 /label= signal_peptide
 FT /label= mature_protein
 PN WO200020577-A1.
 XX
 PD 13-APR-2000.
 XX
 PF 05-OCT-1999; 99WO-US023240.
 XX
 PR 06-OCT-1998; 98US-0103438P.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Tosato G, Pike SE, Yao L;
 DR WPI; 2000-303767/26.
 DR N-PSDB; AAA09346, AAA09347.
 XX
 PT Inhibiting endothelial cell growth and angiogenesis using calreticulin,
 useful for suppressing tumor growth.
 XX
 PS Disclosure; Page 79-80; 99pp; English.
 CC A novel method of inhibiting endothelial cell growth comprises contacting
 the cells with calreticulin (or its fragments/variants). Fragments of
 calreticulin causes at least 40% inhibition of angiogenesis, tumor growth
 and/or endothelial cell growth (claimed). The method may be used for
 inhibiting angiogenesis in a patient. The angiogenesis is associated with
 a disease other than a tumor that is associated with neovascularization
 (e.g. diabetic neuropathy, retrolental fibroplasia, trachoma, neovascular
 glaucoma, psoriasis, angiofibromas, immune inflammation,
 CC atherosclerosis, excessive wound repair, retinal neovascularization,
 CC macular degeneration, corneal graft rejection, contact lens overwear,
 CC Crohn's disease, non-immune inflammation, rheumatoid arthritis, systemic
 CC lupus erythromatosus, thyroiditis, Goodpasture's syndrome, systemic
 CC vasculitis, scleroderma, Sjorgen's syndrome, sarcoidosis and primary
 CC biliary cirrhosis). The method may also be used for treating/inhibiting
 tumor growth especially Kaposi's sarcoma (claimed)
 XX
 SQ Sequence 417 AA;

Query Match 100.0%; Score 318; DB 3; Length 417;
 Best Local Similarity 100.0%; Pred. No. 3.7e-36;
 Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPGTKVHVIFNYKGNVLINKDIRCKDDEFTHLTYLIVRPDNTYEVKIDNSQVSGSLE 60
 |||||
 Db 138 GPGTKVHVIFNYKGNVLINKDIRCKDDEFTHLTYLIVRPDNTYEVKIDNSQVSGSLE 197

RESULT 12
 AAU77712
 ID AAU77712 standard; protein; 417 AA.
 XX
 AC AAU77712;
 XX
 DT 05-JUN-2002 (first entry)
 XX
 DE Human calreticulin (CRT).
 XX
 KW Calreticulin; CRT; endoplasmic reticulum chaperone polypeptide;
 cytostatic; vaccine; human papillomavirus 16; HPV 16; E7; DNA vaccine;
 KW enhanced antigen-specific immune response; cytotoxic T lymphocyte;
 tumour; cancer; cervical cancer.
 XX
 OS Homo sapiens.
 XX
 PN WO200212281-A2.
 XX
 PD 14-FEB-2002.
 XX
 PF 02-AUG-2001; 2001WO-US024134.
 XX
 PR 03-AUG-2000; 2000US-0222902P.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS.
 XX
 PI Wu T, Hung C;
 DR WPI; 2002-257463/30.
 DR N-PSDB; ABK11662.
 XX
 PT New nucleic acids encoding a fusion polypeptide comprising an endoplasmic
 reticulum chaperone polypeptide linked to an antigenic polypeptide,
 PT useful as a vaccine for inducing antigen-specific immune responses.
 XX
 PS Disclosure; Page 27; 71pp; English.
 CC The invention describes a nucleic acid molecule (I) encoding a fusion
 polypeptide comprising a first polypeptide domain comprising an
 endoplasmic reticulum chaperone polypeptide e.g. calreticulin (CRT) and a
 second polypeptide domain comprising at least one antigenic peptide e.g.
 Human papillomavirus 16 (HPV 16) E7. The nucleic acid is useful as a
 CC vaccine (DNA vaccine) for inducing enhanced antigen-specific immune
 CC responses, particularly those mediated by cytotoxic T lymphocytes. The
 CC nucleic acid and compositions comprising the nucleic acid is also useful
 CC for inhibiting the growth of tumours and cancers e.g. cervical cancer.
 CC This is the amino acid sequence of the human calreticulin (CRT), an
 CC endoplasmic reticulum protein used in the creation of a DNA vaccine
 XX
 SQ Sequence 417 AA;

Query Match 100.0%; Score 318; DB 5; Length 417;
 Best Local Similarity 100.0%; Pred. No. 3.7e-36;
 Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPGTKVHVIFNYKGNVLINKDIRCKDDEFTHLTYLIVRPDNTYEVKIDNSQVSGSLE 60
 |||||
 Db 138 GPGTKVHVIFNYKGNVLINKDIRCKDDEFTHLTYLIVRPDNTYEVKIDNSQVSGSLE 197

RESULT 13
 AA24591

ID AAE24591 standard; protein; 417 AA.
XX
AC AAE24591;
XX
DT 04-OCT-2002 (first entry)
XX
DE Human calreticulin protein.
XX
KW Human; calreticulin; antisense compound; hyperproliferative disorder;
KW cancer; autoimmune disease; viral infection; cardiovascular disease;
KW antisense therapy; cytostatic; immunosuppressive; virucide.
XX
OS Homo sapiens.
XX
PN WO200236743-A2.
XX
PD 10-MAY-2002.
XX
PF 30-OCT-2001; 2001WO-US049045.
XX
PR 30-OCT-2000; 2000US-00702327.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Bennett CF, Cowser LM;
PI WPI; 2002-479759/51.
DR N-PSDB; AAD39469.
XX
XX Novel antisense compound targeted to nucleic acid encoding calreticulin,
PT useful for treating a human having disease or condition associated with
PT calreticulin e.g. cancer, viral infection, autoimmune disease.
XX
PS Disclosure; Page 88-90; 109pp; English.
XX
CC The invention relates to antisense compounds, compositions and methods
CC for modulating the expression of calreticulin. The compositions comprise
CC antisense compounds, particularly antisense oligonucleotides, targeted
CC to nucleic acids encoding calreticulin. The antisense compound is useful
CC for inhibiting the expression of calreticulin in human cells or tissues.
CC It is also useful for treating a human having a disease or condition
CC associated with calreticulin, e.g., hyperproliferative disorder e.g.
CC cancer, autoimmune disease, viral infection or cardiovascular disease, by
CC inhibiting expression of calreticulin. It is useful for diagnostics,
CC therapeutics, prophylaxis and as research reagents and kits. It is also
CC used in antisense therapy. The present sequence is human calreticulin
CC protein. This sequence is used in the exemplification of the invention
XX
SQ Sequence 417 AA;
Query Match 100.0%; Score 318; DB 5; Length 417;
Best Local Similarity 100.0%; Pred. No. 3.7e-36;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GPGTKKVVHVFNYKGNVINKDKRCKDDEFTHTLTVLRPDNTYEVKIDNSQVSGSLE 60
DB 138 GPGTKKVVHVFNYKGNVINKDKRCKDDEFTHTLTVLRPDNTYEVKIDNSQVSGSLE 197
RESULT 14
AAE18851
ID AAE18851 standard; protein; 417 AA.
XX
AC AAE18851;
XX
DT 17-MAY-2002 (first entry)
XX
DE Human calreticulin protein.
XX
KW Human; prostate cancer; calreticulin; TID-1 protein; TRAITS protein;
KW androgen action pathway; cell proliferation; kidney cancer; lymphoma;
KW epithelium-derived carcinoma; leukaemia; vaccine; gene therapy;
KW cytostatic; U19 protein.

XX Homo sapiens.
OS
XX Key Location/Qualifiers
XX Domain 98..170
FT /label= N-terminal_domain
FT Region 98..103
FT /label= Alpha_helix
FT Region 149..154
FT /label= Alpha_helix
FT Domain 171..285
FT /note= "Proline-rich domain (P domain)"
FT Domain 286..397
FT /label= C-terminal_domain
XX
XX WO200206327-A2.
XX
XX 24-JAN-2002.
XX
XX 17-JUL-2001; 2001WO-US022357.
XX
XX 17-JUL-2000; 2000US-0218761P.
XX
XX 16-JUL-2001; 2001US-00906393.
XX
XX (NOUN) UNIV NORTHWESTERN.
XX
XX Wang Z, Xiao W;
XX WPI; 2002-179780/23.
XX N-PSDB; AAD29931.
XX
XX Identifying a subject that is likely to have aggressive form of prostate
XX cancer, involves comparing calreticulin levels in prostate specimen of
XX the subject and in benign prostatic epithelial cells of the same subject.
XX
XX Disclosure; Page 146-148; 149pp; English.
XX
XX The present invention relates to methods of distinguishing aggressive
XX forms of prostate cancer from non-aggressive forms. The method involves
XX comparing the level of calreticulin in prostate specimen and in benign
XX prostatic epithelial cells of a subject. The invention particularly
XX relates to two proteins, namely calreticulin and TID-1 (TRAITS; U19) that
XX are down-regulated in aggressive forms of prostate cancer but not in
XX slowly progressing prostate cancer. They play important roles in the part
XX of androgen action pathway that suppresses cell proliferation and/or
XX prevents prostate cancer. The method is useful for identifying a subject
XX who is likely to have an aggressive form of prostate cancer. The
XX invention further relates to a method of identifying a subject with a
XX slow growing form of prostate cancer. TID-1 sequences are useful for
XX treating cancers such as epithelium-derived carcinomas, kidney cancers,
XX lymphomas, leukaemias and prostate cancers. Sequences of the invention
XX are used as vaccines and in gene therapy. The present sequence is human
XX calreticulin protein
XX
SQ Sequence 417 AA;
Query Match 100.0%; Score 318; DB 5; Length 417;
Best Local Similarity 100.0%; Pred. No. 3.7e-36;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GPGTKKVVHVFNYKGNVINKDKRCKDDEFTHTLTVLRPDNTYEVKIDNSQVSGSLE 60
DB 138 GPGTKKVVHVFNYKGNVINKDKRCKDDEFTHTLTVLRPDNTYEVKIDNSQVSGSLE 197
RESULT 15
ABE82384
ID ABE82384 standard; protein; 417 AA.
XX
XX ABE82384;
XX AC
XX 08-JAN-2003 (first entry)
XX
XX

DE Human calreticulin (CRT) protein.
 XX Immunogenicity; cytostatic; virucide; protozoacide; antibacterial; CTL;
 KW hepatotropic; anti-HIV; vaccine. cytotoxic T lymphocyte; tumour; CRT;
 KW calreticulin; human.
 XX Homo sapiens.
 XX WO200274920-A2.
 XX 26-SEP-2002.
 XX 19-MAR-2002; 2002WO-US008033.
 XX 16-MAR-2001; 2001US-0276854P.
 XX (UYJO) UNIV JOHNS HOPKINS.
 XX Wu T, Hung C;
 PI
 XX WPI; 2002-740856/80.
 DR N-PSDB; ABV73173.
 XX
 PT New nucleic acid molecule encoding an antigenic fusion polypeptide useful
 PT as vaccines for enhancing or inducing immune responses, primarily
 PT cytotoxic T lymphocytes (CTL) responses to specific antigens such as
 PT tumor or viral antigens.
 XX
 PS Disclosure; Page 27; 93pp; English.
 XX
 CC The invention relates to a nucleic acid molecule that encodes a fusion
 CC polypeptide, comprising a first nucleic acid sequence encoding a
 CC polypeptide that comprises at least one immunogenicity-potentiating
 CC polypeptide, optionally, fused in frame with the nucleic acid, a linker
 CC nucleic acid encoding a linker peptide, and a nucleic acid that is linked
 CC in frame to them, and that encodes an antigenic peptide or polypeptide.
 CC The nucleic acid molecule, polypeptides and vectors are useful as
 CC vaccines for enhancing immune responses, primarily cytotoxic T
 CC lymphocytes (CTL) responses to specific antigens such as tumour or viral
 CC antigens, and for inhibiting growth or preventing re-growth of a tumour.
 CC The packaging cell line is useful for generating alphavirus replicon
 CC particles without contamination from replicon-competent virus. The
 CC pathogenic organisms include viruses such as human papilloma virus (HPV),
 CC hepatitis B virus, hepatitis C virus, human immunodeficiency virus,
 CC Epstein Barr virus and herpes simplex virus, intracellular parasites such
 CC as malaria, and bacteria that grow intracellularly such as mycobacteria
 CC and listeria. The present sequence represents a human calreticulin (CRT)
 XX
 SQ Sequence 417 AA;
 Query Match 100.0%; Score 318; DB 5; Length 417;
 Best Local Similarity 100.0%; Pred. No. 3,7e-36;
 Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GPGTKKHVIFNYKGNVLINKRCKDDETHLYTLIVRPDNTYEVKIDNSQVESGSL 60
 D5 138 GPGTKKHVIFNYKGNVLINKRCKDDETHLYTLIVRPDNTYEVKIDNSQVESGSL 197

Search completed: October 4, 2004, 13:03:31
 Job time : 45.5294 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 4, 2004, 13:01:22 ; Search time 13.4118 Seconds
(without alignments)
230.958 Million cell updates/sec

Title: US-09-807-148-8

Perfect score: 318

Sequence: 1 GPGTKVHVIFNYGKGNVLI.....PDNTYEVKIDNSQVSGSLE 60

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA.*
1: /cgm2_6/ptodata/2/iaa/5A COMB.pcp.*
2: /cgm2_6/ptodata/2/iaa/5B COMB.pcp.*
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5: /cgm2_6/ptodata/2/iaa/PTCUS COMB.pcp.*
6: /cgm2_6/ptodata/2/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	318	100.0	61	4	US-09-828-000-8
2	318	100.0	180	4	US-09-828-000-3
3	318	100.0	416	4	US-09-828-000-2
4	235	73.9	61	4	US-09-828-000-4
5	189	59.4	35	4	US-09-828-000-7
6	177	55.7	415	3	US-08-675-816-2
7	142	44.7	27	4	US-09-828-000-5
8	115	36.2	593	1	US-08-296-362-2
9	107	33.6	610	4	US-09-976-594-947
10	96	30.2	18	4	US-09-828-000-6
11	79	24.8	542	3	US-08-675-816-6
12	61.5	19.3	582	3	US-08-906-865-3
13	61.5	19.3	582	4	US-09-129-668-3
14	57.5	18.1	126	4	US-09-732-210-1163
15	55	17.3	588	4	US-09-252-991A-18861
16	54.5	17.1	410	2	US-08-723-415B-10
17	54.5	17.1	410	3	US-09-189-627A-10
18	54.5	17.1	410	4	US-09-710-861-10
19	54	17.0	405	1	US-07-829-954-2
20	54	17.0	405	1	US-07-994-423-2
21	54	17.0	405	1	US-08-421-891-2
22	54	17.0	474	4	US-09-134-001C-3176
23	54	17.0	816	1	US-08-190-802A-54
24	54	17.0	816	3	US-08-477-346-54
25	54	17.0	816	4	US-08-473-089-54
26	54	17.0	816	4	US-08-487-072A-54
27	54	17.0	1009	4	US-09-693-146-4

28 53.5 16.8 279 2 US-08-701-191A-23 Sequence 23, Appl
29 53.5 16.8 279 4 US-09-864-526-23 Sequence 23, Appl
30 53.5 16.8 355 1 US-08-292-549-6 Sequence 6, Appl
31 53.5 16.8 355 3 US-09-006-353A-14 Sequence 14, Appl
32 53.5 16.8 355 4 US-09-573-986-14 Sequence 14, Appl
33 53.5 16.8 812 1 US-08-446-794A-4 Sequence 4, Appl
34 53.5 16.8 943 4 US-09-540-236-3458 Sequence 3458, Ap
35 53.5 16.8 984 2 US-08-673-789-9 Sequence 9, Appl
36 53.5 16.8 984 2 US-08-449-645A-19 Sequence 19, Appl
37 53.5 16.8 984 2 US-08-702-367A-19 Sequence 19, Appl
38 53.5 16.8 984 5 FCT-US95-04681-19 Sequence 19, Appl
39 53 16.7 91 4 US-09-134-001C-2969 Sequence 2969, Ap
40 53 16.7 410 2 US-08-723-415B-11 Sequence 11, Appl
41 53 16.7 410 2 US-08-428-131-2 Sequence 2, Appl
42 53 16.7 410 2 US-08-602-846-2 Sequence 2, Appl
43 53 16.7 410 3 US-09-078-596-2 Sequence 2, Appl
44 53 16.7 410 3 US-09-189-627A-11 Sequence 11, Appl
45 53 16.7 410 4 US-09-710-861-11 Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-09-828-000-8
; Sequence 8, Application US/09828000
; Patent No. 6596690
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/09/828,000
; CURRENT FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Fragment 5
US-09-828-000-8

Query Match 100.0%; Score 318; DB 4; Length 61;
Best Local Similarity 100.0%; Pred. No. 2.1e-36;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPGTKVHVIFNYGKGNVLIKDKDEFTHTLYLIVRPDNTYEVKIDNSQVSGSLE 60
Db 2 GPGTKVHVIFNYGKGNVLIKDKDEFTHTLYLIVRPDNTYEVKIDNSQVSGSLE 61

RESULT 2
US-09-828-000-3
; Sequence 3, Application US/09828000
; Patent No. 6596690
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/09/828,000
; CURRENT FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Vasostatin
US-09-828-000-3

Query Match 100.0%; Score 318; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 8.6e-36;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPGTKVHVIFNYGKGNVLIKDKDEFTHTLYLIVRPDNTYEVKIDNSQVSGSLE 60

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Db 121 GPGTKKHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSLE 180
|||||
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Best Local Similarity 100.0%; Pred. No. 5.1e-25;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPGTKKHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSLE 60
Db 138 GPGTKKHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSLE 197
|||||

RESULT 4
US-09-828-000-4
; Sequence 4, Application US/09828000
; Patent No. 6596690
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/09/828,000
; CURRENT FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Calreticulin
US-09-828-000-2
Query Match 100.0%; Score 318; DB 4; Length 416;
Best Local Similarity 100.0%; Pred. No. 2.5e-35;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPGTKKHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSLE 60
Db 138 GPGTKKHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSLE 197
|||||

RESULT 5
US-09-828-000-7
; Sequence 7, Application US/09828000
; Patent No. 6596690
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/09/828,000
; CURRENT FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 35
; TYPE: PRT
US-09-828-000-4
Query Match 73.9%; Score 235; DB 4; Length 61;
Best Local Similarity 100.0%; Pred. No. 5.1e-25;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPGTKKHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSLE 60
Db 19 GPGTKKHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSLE 61
|||||

RESULT 6
US-08-675-816-2
; Sequence 2, Application US/08675816
; Patent No. 6171864
; GENERAL INFORMATION:
; APPLICANT: Coughlan, Sean J.
; TITLE OF INVENTION: CALRETICULIN AND CALNEXIN GENES AND PROMOTER REGIONS AND USES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Seed and Berry
; STREET: 701 Fifth Ave. Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/675,816
; FILING DATE: 05-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6171864tenburg, Carol
; REGISTRATION NUMBER: 39,317
; REFERENCE/DOCKET NUMBER: 750027.401
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206-622-4900
; TELEFAX: (206)-682-6031
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 415 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-675-816-2
Query Match 55.7%; Score 177; DB 3; Length 415;
Best Local Similarity 52.5%; Pred. No. 5.3e-16;
Matches 31; Conservative 11; Mismatches 17; Indels 0; Gaps 0;

QY 1 GPGTKKHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSLE 59
Db 139 GYSTKKVHALNNDNTNHLIKKEVPCETDQLTHYTLIVREDATYSLIDNVEKQTGSL 197
|||||

RESULT 7
US-09-828-000-5
; Sequence 5, Application US/09828000
; Patent No. 6596690
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/09/828,000
; CURRENT FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
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; ORGANISM: Fragment 4
US-09-828-000-7
Query Match 59.4%; Score 189; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 5e-19;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSLE 43
Db 1 VIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSLE 35
|||||

RESULT 6
US-08-675-816-2
; Sequence 2, Application US/08675816
; Patent No. 6171864
; GENERAL INFORMATION:
; APPLICANT: Coughlan, Sean J.
; TITLE OF INVENTION: CALRETICULIN AND CALNEXIN GENES AND PROMOTER REGIONS AND USES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Seed and Berry
; STREET: 701 Fifth Ave. Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/675,816
; FILING DATE: 05-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6171864tenburg, Carol
; REGISTRATION NUMBER: 39,317
; REFERENCE/DOCKET NUMBER: 750027.401
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206-622-4900
; TELEFAX: (206)-682-6031
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 415 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-675-816-2
Query Match 55.7%; Score 177; DB 3; Length 415;
Best Local Similarity 52.5%; Pred. No. 5.3e-16;
Matches 31; Conservative 11; Mismatches 17; Indels 0; Gaps 0;

QY 1 GPGTKKHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSLE 59
Db 139 GYSTKKVHALNNDNTNHLIKKEVPCETDQLTHYTLIVREDATYSLIDNVEKQTGSL 197
|||||

RESULT 7
US-09-828-000-5
; Sequence 5, Application US/09828000
; Patent No. 6596690
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/09/828,000
; CURRENT FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
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; SEQ ID NO 5
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Fragment 2
US-09-828-000-5

Query Match      44.7%; Score 142; DB 4; Length 27;
Best Local Similarity 100.0%; Pred. No. 1e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFGTKKHVIFNYKGNVINKDIRC 26
Db 2 GFGTKKHVIFNYKGNVINKDIRC 27

RESULT 8
US-08-296-362-2
; Sequence 2, Application US/08296362
; Patent No. 5691306
; GENERAL INFORMATION:
; APPLICANT: Bergeron, John J.M.
; APPLICANT: Thomas, David Y.
; APPLICANT: Wada, Ikuro
; TITLE OF INVENTION: METHODS OF DETECTION AND TREATMENT OF
; TITLE OF INVENTION: PROTEIN TRAFFICKING DISORDERS AND INCREASING SECRETORY
; TITLE OF INVENTION: PROTEIN PRODUCTION
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESS: SEED AND BERRY
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/296,362
; FILING DATE: 25-AUG-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Deehr, Manva S.
; REGISTRATION NUMBER: 37,120
; REFERENCE/DOCKET NUMBER: 690066.401C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; TELEX: 3723836
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 593 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-296-362-2

Query Match      36.2%; Score 115; DB 1; Length 593;
Best Local Similarity 37.5%; Pred. No. 2.7e-07;
Matches 24; Conservative 12; Mismatches 18; Indels 10; Gaps 1;

QY 6 KHVIFNYKGNVINKDIRC-----DSEFTHLYTLIVRPDNTYEVKIDNSQVE 55
Db 200 KLHFIFRHKPXTGTVFEKHAKRPDADLKTYFTDKKTHLYTLINPDNSFEILVDQSI 259
QY 56 SGSL 59
Db 260 SGSL 263

RESULT 9
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US-09-976-594-947
; Sequence 947, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 947
; LENGTH: 610
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 3876162CD1
US-09-976-594-947

Query Match      33.6%; Score 107; DB 4; Length 610;
Best Local Similarity 35.9%; Pred. No. 3.4e-06;
Matches 23; Conservative 11; Mismatches 20; Indels 10; Gaps 1;

QY 6 KHVIFNYKGNVINKDIRC-----DSEFTHLYTLIVRPDNTYEVKIDNSQVE 55
Db 190 KLHFIFRHKPXTGTVFEKHAKRPDADLKTYFTDKKTHLYTLINPDNSFEILVDQSI 249
QY 56 SGSL 59
Db 250 KGSL 253

RESULT 10
US-09-828-000-6
; Sequence 6, Application US/09828000
; Patent No. 6596690
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/09/828,000
; CURRENT FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 6
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Fragment 3
US-09-828-000-6

Query Match      30.2%; Score 96; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VIFNYKGNVINKDIRC 26
Db 1 VIFNYKGNVINKDIRC 18

RESULT 11
US-08-675-816-6
; Sequence 6, Application US/08675816
; Patent No. 6171864
; GENERAL INFORMATION:
; APPLICANT: Coughlan, Sean J.
; APPLICANT: Winfrey, Jr., Ron J.
; TITLE OF INVENTION: CALRETICULIN AND CALNEXIN GENES AND PROMOTER REGIONS AND USSES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
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; ADDRESSEE: Seed and Berry
; STREET: 701 Fifth Ave. Suite 5300
; CITY: Seattle
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/675,816
; FILING DATE: 05-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6171864tenburg, Carol
; REGISTRATION NUMBER: 39,317
; REFERENCE/DOCKET NUMBER: 750027.401
; TELEPHONE: (206)-622-4900
; TELEFAX: (206)-682-6031
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 542 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-675-816-6

Query Match 24.8%; Score 79; DB 3; Length 542;
Best Local Similarity 30.2%; Pred. No. 0.02;
Matches 19; Conservative 10; Mismatches 24; Indels 10; Gaps 3;

QY 1 GP-----GKQVHVFNYKG--KVLINKDIR----CKDBEFHLYTLIVRPDNTYEVKID 50
DB 143 GPDKCGATNKVHFILKHKPKSGEYIEHLKYPSPVSKLTHVYTAILKPDNEURLILD 202
QY 51 NSQ 53
DB 203 GEE 205

RESULT 12
US-08-906-865-3
; Sequence 3, Application US/08906865
; Patent No. 6040168
; GENERAL INFORMATION:
; APPLICANT: Greengard, Paul
; APPLICANT: Porton, Barbara
; APPLICANT: Kao, Hung-Teh
; TITLE OF INVENTION: DNA ENCODING THE HUMAN SYNAPSIN III GENE
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/906,865
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.

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; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 582 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: /desc = "Synapsin IIA"
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; US-08-906-865-3

Query Match 19.3%; Score 61.5; DB 3; Length 582;
Best Local Similarity 40.0%; Pred. No. 5.6;
Matches 14; Conservative 7; Mismatches 13; Indels 1; Gaps 1;

QY 13 YGKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEV 47
DB 130 FRGKKVLGDYDIKVEQAEFSEL-NLVAHADGTAYV 163

RESULT 13
US-09-129-668-3
; Sequence 3, Application US/09129668B
; Patent No. 642901C
; GENERAL INFORMATION:
; APPLICANT: Greengard, Paul
; APPLICANT: Porton, Barbara
; APPLICANT: Kao, Hung-Teh
; TITLE OF INVENTION: DNA ENCODING THE HUMAN SYNAPSIN III GENE AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 600-1-202 CIP
; CURRENT APPLICATION NUMBER: US/09/129,668B
; CURRENT FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 08/906,865
; EARLIER FILING DATE: 1997-08-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 3
; LENGTH: 582
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-129-668-3

Query Match 19.3%; Score 61.5; DB 4; Length 582;
Best Local Similarity 40.0%; Pred. No. 5.6;
Matches 14; Conservative 7; Mismatches 13; Indels 1; Gaps 1;

QY 13 YGKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEV 47
DB 130 FRGKKVLGDYDIKVEQAEFSEL-NLVAHADGTAYV 163

RESULT 14
US-09-732-210-1163
; Sequence 1163, Application US/09732210
; Patent No. 6573361
; GENERAL INFORMATION:
; APPLICANT: Bunkers, Greg J.
; APPLICANT: Liang, Jihong
; APPLICANT: Mittanck, Cindy A.
; APPLICANT: Seale, Jeffrey W.
; APPLICANT: Wu, Yonnie S.
; TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use
; FILE REFERENCE: 38-21(15036)B
; CURRENT APPLICATION NUMBER: US/09/732,210
; CURRENT FILING DATE: 2000-12-07

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; PRIOR APPLICATION NUMBER: US 60/169,513
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: US 60/169,340
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 1753
; SEQ ID NO 1163
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Porphyra purpurea
US-09-732-210-1163

Query Match 18.1%; Score 57.5; DB 4; Length 126;
Best Local Similarity 21.9%; Pred. No. 2.8;
Matches 16; Conservative 20; Mismatches 20; Indels 17; Gaps 4;

QY 2 PGTKKVHVFENY-----KGNVL-----INKDIRCK---DDEFTHTLYTLIVRPDNTYEV 47
DB 10 PANKREIALTYIGIGLSRSKEILKKTNDIDIRCONLNDDQIVSIREIL---ESSYQI 65

QY 48 KIDNSQVSGSLE 60
DB 67 EGDKKRFESMSIK 79

RESULT 15

US-09-252-991A-18861
; Sequence 18861, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18861
; LENGTH: 588
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18861

Query Match 17.3%; Score 55; DB 4; Length 588;
Best Local Similarity 48.0%; Pred. No. 44;
Matches 12; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 14 KGNVLINKDIRCKDDEFTHTLYTLI 38
DB 364 RGGDPLLGKDIRKLDVDDVDTAL 388

Search completed: October 4, 2004, 13:07:21
Job time : 14.4116 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 4, 2004, 13:06:03 ; Search time 44.1176 Seconds
(without alignments)
437.647 Million cell updates/sec

Title: US-09-807-148-8
Perfect score: 318
Sequence: 1 GPCTKKVHVFYFNKGNVLI.....PNTVEVKIDNSQVSGSLE 60

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1351062 seqs, 321799191 residues

Total number of hits satisfying chosen parameters: 1351062

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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2: /cgn2_6/ptodata/1/pubpa/PCT_NEW_PUB.pep:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	318	100.0	61	10	US-09-828-000-8
2	318	100.0	61	15	US-10-405-588-8
3	318	100.0	180	10	US-09-828-000-3
4	318	100.0	180	15	US-10-405-588-3
5	318	100.0	416	10	US-09-828-000-2
6	318	100.0	416	14	US-10-316-253-2
7	318	100.0	416	14	US-10-316-253-4
8	318	100.0	416	14	US-10-316-253-6
9	318	100.0	416	15	US-10-405-588-2
10	318	100.0	417	10	US-09-906-393A-36
11	318	100.0	417	14	US-10-161-959-29
12	318	100.0	417	15	US-10-367-093-14
13	235	73.9	61	10	US-09-828-000-4
14	235	73.9	61	15	US-10-405-588-4
15	210.5	66.2	395	15	US-10-369-493-6343

16	204	64.2	210	16	US-10-767-701-55877	Sequence 55877, A
17	189	59.4	35	10	US-09-828-000-7	Sequence 7, Appli
18	189	59.4	35	15	US-10-405-588-7	Sequence 7, Appli
19	179	56.3	346	12	US-10-425-114-48930	Sequence 48930, A
20	179	56.3	421	16	US-10-767-701-46544	Sequence 46544, A
21	179	56.3	435	12	US-10-425-114-70304	Sequence 70304, A
22	179	56.3	442	16	US-10-437-963-114914	Sequence 114914, A
23	179	56.3	667	16	US-10-437-963-114860	Sequence 114860, A
24	177	55.7	388	12	US-10-425-114-46405	Sequence 46405, A
25	177	55.7	391	12	US-10-425-114-69619	Sequence 69619, A
26	177	55.7	442	12	US-10-425-114-46869	Sequence 46869, A
27	176	55.3	290	12	US-10-425-114-44768	Sequence 44768, A
28	176	55.3	422	15	US-10-424-599-27745	Sequence 27745, A
29	175	55.0	390	15	US-10-161-327-46	Sequence 46, Appl
30	174	54.7	425	16	US-10-437-963-12222	Sequence 12222, A
31	171	53.8	94	14	US-10-029-386-32394	Sequence 32394, A
32	171	53.8	391	12	US-10-424-599-190956	Sequence 190956, A
33	171	53.8	391	12	US-10-425-114-46228	Sequence 46228, A
34	171	53.8	391	12	US-10-425-114-55995	Sequence 55995, A
35	171	53.8	420	12	US-10-424-599-190958	Sequence 190958, A
36	171	53.8	424	16	US-10-437-963-201427	Sequence 201427, A
37	171	53.8	434	12	US-10-425-114-70140	Sequence 70140, A
38	171	53.8	439	12	US-10-425-114-65495	Sequence 65495, A
39	170	53.5	247	12	US-10-424-599-153809	Sequence 153809, A
40	170	53.5	372	12	US-10-425-114-44621	Sequence 44621, A
41	170	53.5	372	12	US-10-425-114-54997	Sequence 54997, A
42	170	53.5	418	12	US-10-424-599-153808	Sequence 153808, A
43	170	53.5	420	9	US-09-844-006A-2	Sequence 2, Appli
44	170	53.5	424	16	US-10-437-963-201420	Sequence 201420, A
45	166	52.2	279	16	US-10-767-701-39041	Sequence 39041, A

ALIGNMENTS

RESULT 1

US-09-828-000-8
; Sequence 8, Application US/09828000
; Publication No. US20030078198A1
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/09/828,000
; CURRENT FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Fragment 5
US-09-828-000-8

Query Match 100.0%; Score 318; DB 10; Length 61;
Best Local Similarity 100.0%; Pred. No. 1.5e-34;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPCTKKVHVFYFNKGNVLIINKDIRCKDDEFTLYLIVRPDNTVEVKIDNSQVSGSLE 60
DB 2 GPCTKKVHVFYFNKGNVLIINKDIRCKDDEFTLYLIVRPDNTVEVKIDNSQVSGSLE 61

RESULT 2

US-10-405-588-8
; Sequence 8, Application US/10405588
; Publication No. US20030216299A1
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/10/405,588
; CURRENT FILING DATE: 2003-04-01
; PRIOR APPLICATION NUMBER: US/09/828,000

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; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Fragment 5
US-10-405-588-8

Query Match      100.0%; Score 318; DB 15; Length 61;
Best Local Similarity 100.0%; Pred. No. 1.5e-34;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPGTKKVHVIFNYKGNVLINKDIRCKDDEFTHLTYLIVRPDNTYEVKIDNSQVSGSLE 60
Db 2 GPGTKKVHVIFNYKGNVLINKDIRCKDDEFTHLTYLIVRPDNTYEVKIDNSQVSGSLE 61

RESULT 3
US-09-828-000-3
; Sequence 3, Application US/09828000
; Publication No. US20030078198A1
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/09/828,000
; CURRENT FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Vasostatin
US-09-828-000-3

Query Match      100.0%; Score 318; DB 10; Length 180;
Best Local Similarity 100.0%; Pred. No. 6.1e-34;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPGTKKVHVIFNYKGNVLINKDIRCKDDEFTHLTYLIVRPDNTYEVKIDNSQVSGSLE 60
Db 121 GPGTKKVHVIFNYKGNVLINKDIRCKDDEFTHLTYLIVRPDNTYEVKIDNSQVSGSLE 180

RESULT 4
US-10-405-588-3
; Sequence 3, Application US/10405588
; Publication No. US20030216299A1
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/10/405,588
; PRIOR FILING DATE: 2003-04-01
; PRIOR APPLICATION NUMBER: US/09/828,000
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Vasostatin
US-10-405-588-3

Query Match      100.0%; Score 318; DB 15; Length 180;
Best Local Similarity 100.0%; Pred. No. 6.1e-34;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPGTKKVHVIFNYKGNVLINKDIRCKDDEFTHLTYLIVRPDNTYEVKIDNSQVSGSLE 60
Db 121 GPGTKKVHVIFNYKGNVLINKDIRCKDDEFTHLTYLIVRPDNTYEVKIDNSQVSGSLE 180

RESULT 5
US-09-828-000-2
; Sequence 2, Application US/09828000
; Publication No. US20030078198A1
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/09/828,000
; CURRENT FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Calcitriculin
US-09-828-000-2

Query Match      100.0%; Score 318; DB 10; Length 416;
Best Local Similarity 100.0%; Pred. No. 1.8e-33;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPGTKKVHVIFNYKGNVLINKDIRCKDDEFTHLTYLIVRPDNTYEVKIDNSQVSGSLE 60
Db 138 GPGTKKVHVIFNYKGNVLINKDIRCKDDEFTHLTYLIVRPDNTYEVKIDNSQVSGSLE 197

RESULT 6
US-10-316-253-2
; Sequence 2, Application US/10316253
; Publication No. US20030162706A1
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Peters, Kevin
; APPLICANT: Thompson, Larry
; APPLICANT: Wang, Feng
; APPLICANT: Greis, Kenneth
; TITLE OF INVENTION: Angiogenesis Modulating Proteins
; FILE REFERENCE: 8865M
; CURRENT APPLICATION NUMBER: US/10/316,253
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: US 60/355,295
; PRIOR FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-316-253-2

Query Match      100.0%; Score 318; DB 14; Length 416;
Best Local Similarity 100.0%; Pred. No. 1.8e-33;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPGTKKVHVIFNYKGNVLINKDIRCKDDEFTHLTYLIVRPDNTYEVKIDNSQVSGSLE 60
Db 138 GPGTKKVHVIFNYKGNVLINKDIRCKDDEFTHLTYLIVRPDNTYEVKIDNSQVSGSLE 197

RESULT 7
US-10-316-253-4
; Sequence 4, Application US/10316253
; Publication No. US20030162706A1
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Peters, Kevin
; APPLICANT: Thompson, Larry
; APPLICANT: Wang, Feng
; APPLICANT: Greis, Kenneth
; TITLE OF INVENTION: Angiogenesis Modulating Proteins
; FILE REFERENCE: 8865M
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; CURRENT APPLICATION NUMBER: US/10/316,253
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: US 60/355,295
; PRIOR FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-316-253-4

Query Match      100.0%; Score 318; DB 14; Length 416;
Best Local Similarity 100.0%; Pred. No. 1.8e-33;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPGTKKVHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSLE 60
Db 138 GPGTKKVHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSLE 197

RESULT 8
US-10-316-253-6
; Sequence 6, Application US/10316253
; Publication No. US20030162706A1
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Peters, Kevin
; APPLICANT: Thompson, Larry
; APPLICANT: Wang, Feng
; APPLICANT: Greis, Kenneth
; TITLE OF INVENTION: Angiogenesis Modulating Proteins
; FILE REFERENCE: 8865M
; CURRENT APPLICATION NUMBER: US/10/316,253
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: US 60/355,295
; PRIOR FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 6
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-316-253-6

Query Match      100.0%; Score 318; DB 14; Length 416;
Best Local Similarity 100.0%; Pred. No. 1.8e-33;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPGTKKVHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSLE 60
Db 138 GPGTKKVHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSLE 197

RESULT 9
US-10-405-588-2
; Sequence 2, Application US/10405588
; Publication No. US20030216299A1
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/10/405,588
; CURRENT FILING DATE: 2003-04-01
; PRIOR APPLICATION NUMBER: US/09/828,000
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Calreticulin
US-10-405-588-2
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Query Match      100.0%; Score 318; DB 15; Length 416;
Best Local Similarity 100.0%; Pred. No. 1.8e-33;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPGTKKVHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSLE 60
Db 138 GPGTKKVHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSLE 197

RESULT 10
US-09-906-393A-36
; Sequence 36, Application US/09906393A
; Publication No. US20030039970A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Zhou
; APPLICANT: Xiao, Wuhan
; TITLE OF INVENTION: METHOD OF PROGNOSING CANCER AND THE PROTEINS INVOLVED
; FILE REFERENCE: 1720-1-001CIP
; CURRENT APPLICATION NUMBER: US/09/906,393A
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/218,761
; PRIOR FILING DATE: 2000-07-17
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 36
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-906-393A-36

Query Match      100.0%; Score 318; DB 10; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.8e-33;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPGTKKVHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSLE 60
Db 138 GPGTKKVHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSLE 197

RESULT 11
US-10-161-959-29
; Sequence 29, Application US/10161959
; Publication No. US20030096748A1
; GENERAL INFORMATION:
; APPLICANT: Holoshitz, Joseph
; APPLICANT: Ling, Song
; TITLE OF INVENTION: Methods and Compositions for the Treatment of Diseases Associated with Signal Transduction Aberrations
; FILE REFERENCE: UM-07135
; CURRENT APPLICATION NUMBER: US/10/161,959
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: 60/295,691
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 29
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-161-959-29

Query Match      100.0%; Score 318; DB 14; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.8e-33;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPGTKKVHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSLE 60
Db 138 GPGTKKVHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSLE 197
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RESULT 12
US-10-367-093-14
; Sequence 14, Application US/10367093
; Publication No. US20030216315A1
; GENERAL INFORMATION:
; APPLICANT: Duke University
; APPLICANT: Nicchitta, Chris
; APPLICANT: Baker-LeFain, Julie
; TITLE OF INVENTION: MODULATION OF IMMUNE RESPONSE BY NON-PEPTIDE BINDING STRESS RESPO
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 180/145
; CURRENT APPLICATION NUMBER: US/10/367,093
; CURRENT FILING DATE: 2003-02-13
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-367-093-14

Query Match      73.9%; Score 318; DB 15; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.8e-33;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPCTKKVHVFNYKGNVLINKDIRCKDDEFTLHYTLIVRPDNTYEVKIDNSQVSGSLE 60
Db 138 GPCTKKVHVFNYKGNVLINKDIRCKDDEFTLHYTLIVRPDNTYEVKIDNSQVSGSLE 197

RESULT 13
US-09-828-000-4
; Sequence 4, Application US/09828000
; Publication No. US20030078198A1
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/09/828,000
; CURRENT FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Fragment 1
US-09-828-000-4

Query Match      73.9%; Score 235; DB 10; Length 61;
Best Local Similarity 100.0%; Pred. No. 1.6e-23;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPCTKKVHVFNYKGNVLINKDIRCKDDEFTLHYTLIVRPDNTYEVKIDNSQVSGSLE 43
Db 19 GPCTKKVHVFNYKGNVLINKDIRCKDDEFTLHYTLIVRPDNTYEVKIDNSQVSGSLE 61

RESULT 14
US-10-405-588-4
; Sequence 4, Application US/10405588
; Publication No. US20030216299A1
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/10/405,588
; CURRENT FILING DATE: 2003-04-01
; PRIOR APPLICATION NUMBER: US/09/828,000
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 61
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; TYPE: PRT
; ORGANISM: Fragment 1
US-10-405-588-4

Query Match      73.9%; Score 235; DB 15; Length 61;
Best Local Similarity 100.0%; Pred. No. 1.6e-23;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPCTKKVHVFNYKGNVLINKDIRCKDDEFTLHYTLIVRPDNTYEVKIDNSQVSGSLE 60
Db 19 GPCTKKVHVFNYKGNVLINKDIRCKDDEFTLHYTLIVRPDNTYEVKIDNSQVSGSLE 192

RESULT 15
US-10-369-493-6343
; Sequence 6343, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 6343
; LENGTH: 395
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-6343

Query Match      66.2%; Score 210.5; DB 15; Length 395;
Best Local Similarity 66.7%; Pred. No. 3.1e-19;
Matches 40; Conservative 7; Mismatches 12; Indels 1; Gaps 1;

QY 1 GPCTKKVHVFNYKGNVLINKDIRCKDDEFTLHYTLIVRPDNTYEVKIDNSQVSGSLE 60
Db 134 GP-TRRVHVLNKGKNGKLIKEITCKSDDELTHLYTLILNSDNTYEVKIDGESAQTSLE 192

Search completed: October 4, 2004, 13:17:34
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GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: October 4, 2004, 12:55:52 ; Search time 13.0588 seconds
(without alignments)
441.961 Million cell updates/sec

Title: US-09-807-148-8
Perfect score: 318
Sequence: 1 GPQTKKHVIFNYKGNVL.....PDNTYEVKIDNSQVSGSLE 60

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78 : *
1: pir1 : *
2: pir2 : *
3: pir3 : *
4: pir4 : *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	318	100.0	416	1 S06763	calreticulin precu
2	318	100.0	416	2 JH0819	calreticulin precu
3	318	100.0	417	1 A37047	calreticulin precu
4	318	100.0	418	1 A34154	calreticulin precu
5	313	98.4	400	2 S43376	calreticulin, brai
6	313	98.4	421	2 S36799	calreticulin precu
7	281	88.4	405	1 JH0795	calreticulin (clon
8	278	87.4	384	2 S29130	calreticulin precu
9	278	87.4	411	2 S29129	calreticulin homol
10	269	84.6	406	2 A56637	calreticulin precu
11	262	82.4	419	2 S71343	calreticulin precu
12	242	76.1	336	2 A32507	41K larval antigen
13	227	71.4	393	1 A48573	calreticulin autoa
14	210.5	66.2	395	2 S25811	calreticulin precu
15	184	57.9	416	2 T44554	calreticulin - bee
16	179	56.3	421	2 S58170	calreticulin precu
17	177	55.7	415	2 T10172	calreticulin - cas
18	176	55.3	412	2 T05703	calreticulin - bar
19	176	55.3	415	2 T05705	calreticulin - bar
20	172	54.1	425	2 C36605	calreticulin (crt1
21	169	53.1	389	2 T03691	calreticulin - com
22	169	53.1	416	2 T16968	calreticulin cali
23	169	53.1	444	2 H86224	hypothetical prote
24	168	52.8	422	2 T07841	probable calreticu
25	117	36.8	592	2 I53260	calnexin - human
26	117	36.8	592	2 A46673	calnexin precursor
27	116	36.5	591	2 B54354	calnexin precursor
28	116	36.5	591	2 C54354	calnexin precursor
29	115	36.2	593	1 A37273	calnexin precursor

30	114	35.8	582	2 A46637	calnexin homolog S
31	109	34.3	622	2 S71342	calnexin precursor
32	106	33.3	611	2 A53418	calmegin precursor
33	106	33.3	611	2 A54086	calnexin-t - mouse
34	98	30.8	619	2 A40938	hypothetical prote
35	97.5	30.7	560	2 S56142	calcium-binding pr
36	87	27.4	297	2 S70552	calnexin homolog C
37	87	27.4	546	2 T06415	calnexin - soybean
38	84	26.4	356	2 A46164	calnexin - human (
39	82	25.8	530	2 JN0597	calnexin-like prot
40	77	24.2	540	2 T10892	probable calnexin
41	75	23.6	428	2 T03251	calnexin - maize (
42	72	22.6	532	2 T49873	calnexin homolog -
43	64.5	20.3	540	1 J00470	site-specific DNA-
44	64.5	20.3	981	2 T46330	hypothetical prote
45	64	20.1	451	2 T16162	hypothetical prote

ALIGNMENTS

RESULT 1

S06763
calreticulin precursor - mouse
N:Alternate names: 55K calcium-binding reticuloplasmin; calregulin
C:Species: Mus musculus (house mouse)
C:Date: 10-Sep-1999 #sequence-revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S06763; JCI444; FCI233; A57498
R:Smith, M.J.; Koch, G.L.E.
EMBO J. 8, 3581-3586, 1989
A:Title: Multiple zones in the sequence of calreticulin (CRP55, calregulin, HACBP), a m
A:Reference number: S06763; MUID:90059955; PMID:2583110
A:Accession: S06763
A:Molecule type: DNA
A:Residues: 1-416 <SMI>
R:Mazzarella, R.A.; Gold, P.; Cunningham, M.; Green, M.
Gene 120, 217-225, 1992
A:Title: Determination of the sequence of an expressible cDNA clone encoding ERp60/calr
A:Reference number: JCI444; MUID:93013037; PMID:1398135
A:Accession: JCI444
A:Molecule type: mRNA
A:Residues: 1-416 <MAZ>
A:Cross-references: GB:I092988; NID:G193084; PIDN:AAA37569.1; PID:G193085
A:Molecule type: protein
A:Accession: FCI233
A:Residues: 18-41 <MA2>
R:White, T.K.; Zhu, Q.; Tanzer, M.L.
J. Biol. Chem. 270, 15926-15929, 1995
A:Title: Cell surface calreticulin is a putative mannoside lectin which triggers mouse
A:Reference number: A57498; MUID:95332280; PMID:7608143
A:Accession: A57498
A>Status: preliminary
A:Molecule type: Protein
A:Residues: 74-80;142-151;186-193 <WHI>
C:Superfamily: calreticulin
C:Keywords: calcium binding
P:1-17/Domain: signal sequence #status predicted <SIG>
F:18-416/Product: calregulin #status experimental <MAT>
F:13-416/Region: endoplasmic reticulum retention signal

Query Match 100.0%; Score 318; DB 1; Length 416;
Best Local Similarity 100.0%; Pred. No. 6.2e-30;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPQTKKHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSLE 60
Db 138 GPQTKKHVIFNYKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSLE 197

RESULT 2

JH0819
calreticulin precursor - rat

N; Alternate names: calcium-binding protein 3
C: Species: Rattus norvegicus (Norway rat)
C: Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text change 20-Jun-2000
C: Accession: J08819; S1109; S45036; S04867; S39372; A34473; S13045
R: Nakamura, M.; Moriya, M.; Baba, T.; Michikawa, Y.; Yamanobe, T.; Arai, K.; Okinaga, S.
Exp. Cell Res. 205, 101-110, 1993
A: Title: An endoplasmic reticulum protein, calreticulin, is transported into the acrosome
A: Reference number: A49176; MUID: 93202172; PMID: 8453394
A: Accession: J08819
A: Molecule type: mRNA
A: Residues: 1-416 <NAK>
A: Cross-references: GB: D78308; NID: G1089798; PIDN: BAA11345.1; PID: G1845572
A: Accession: A49176
A: Status: preliminary
A: Molecule type: mRNA; protein
A: Residues: 1-416 <NA2>
A: Cross-references: GB: D78308; NID: G1089798; PIDN: BAA11345.1; PID: G1845572
A: Experimental source: Sprague-Dawley, spermatogenic cells
R: Murthy, K.K.; Banville, D.; Srikanth, C.B.; Carrier, F.; Holmes, C.; Bell, A.; Patel, Y.
Nucleic Acids Res. 18, 4933, 1990
A: Title: Structural homology between the rat calreticulin gene product and the Onchocerca
A: Reference number: S11205; MUID: 90370496; PMID: 2395661
A: Accession: S11205
A: Molecule type: mRNA
A: Residues: 1-416 <MUR>
A: Cross-references: EMBL: X53363; NID: G55854; PIDN: CAA37446.1; PID: G55855
R: Nakamura, M.; Michikawa, Y.; Baba, T.; Okinaga, S.; Arai, K.
Biochem. Biophys. Res. Commun. 186, 668-673, 1992
A: Title: Calreticulin is present in the acrosome of spermatozoa of rat testis.
A: Reference number: PC1109; MUID: 92360010; PMID: 1497655
A: Accession: PC1109
A: Molecule type: protein
A: Residues: 18-32 <NAK2>
A: Experimental source: testis, strain Sprague-Dawley
R: Soenichsen, B.; Fueillekrug, J.; van Nguyen, P.; Diekmann, W.; Robinson, D.G.; Mieskes
submitted to the EMBL Data Library, May 1994
A: Description: Retention and retrieval: both mechanisms cooperate to maintain calreticulin
A: Reference number: S45036
A: Accession: S45036
A: Status: preliminary
A: Molecule type: mRNA
A: Residues: 1-416 <SOE>
A: Cross-references: EMBL: X79327; NID: G488840; PIDN: CAA55890.1; PID: G488841
R: Lone, J.C.; Bailly, A.; Latrufile, N.
submitted to the EMBL Data Library, December 1998
A: Reference number: S04867
A: Accession: S04867
A: Molecule type: mRNA
A: Residues: 'R', 270-358, 'AAG', <LON>
A: Cross-references: EMBL: X13702; NID: G56055; PIDN: CAA31987.1; PID: G930260
A: Note: The authors designated the protein as D-beta-hydroxybutyrate dehydrogenase
R: Yokoi, T.; Nagayama, S.; Kajiwara, R.; Kawaguchi, Y.; Horiuchi, R.; Kamataki, T.
Biochim. Biophys. Acta 1158, 339-344, 1993
A: Title: Identification of protein disulfide isomerase and calreticulin as autoimmune an
A: Reference number: S39371; MUID: 94072621; PMID: 8251535
A: Accession: S39371
A: Molecule type: protein
A: Residues: 18-23, 'X', 25-32 <YOK>
R: van, P.N.; Peter, F.; Soeling, H.D.
J. Biol. Chem. 264, 17494-17501, 1989
A: Title: Four intracisternal calcium-binding glycoproteins from rat liver microsomes with
active calcium sequestering rat liver vesicles
A: Reference number: A34473; MUID: 90008920; PMID: 2793869
A: Accession: A34473
A: Status: preliminary
A: Molecule type: protein
A: Residues: 18-36 <VAN>
R: Treves, S.; de Mattei, M.; Lanfredi, M.; Villa, A.; Green, N.M.; MacLennan, D.H.; Meld
Biochem. J. 271, 473-480, 1990
A: Title: Calreticulin is a candidate for a calsequestrin-like function in Ca(2+)-storage
A: Reference number: S13045; MUID: 9105441; PMID: 2241926
A: Accession: S13045

A: Molecule type: protein
A: Residues: 18-29 <TRE>
C: Superfamily: calreticulin
C: Keywords: calcium binding; glycoprotein
F: 1-17/Domain: signal sequence #status predicted <SIG>
F: 18-41/Product: calreticulin #status experimental <MAT>
F: 204-212/Region: nuclear location signal
F: 413-416/Region: endoplasmic reticulum retention signal
F: 344/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 100.0%; Score 318; DB 2; Length 415;
Best Local Similarity 100.0%; Pred. No. 6.2e-30;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CQ 1 GPGTKVHVIFNYKGNVLINKIRCKDDEFTLYTLIVRPDNTYEVKIDNSQVSGSLE 60
|||||
Db 138 GPGTKVHVIFNYKGNVLINKIRCKDDEFTLYTLIVRPDNTYEVKIDNSQVSGSLE 197
RESULT 3
A37047
calreticulin precursor - human
N: Alternate names: 52K ribonucleoprotein autoantigen Ro/SS-A; 60K integrin-binding prote
C: Species: Homo sapiens (man)
C: Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text change 18-Feb-2000
C: Accession: A42330; A37047; A46452; A28812; PH1525; A40346; S11475; T45075
R: McCauliffe, D.P.; Yang, Y.S.; Wilton, J.; Sontheimer, R.D.; Capra, J.D.
J. Biol. Chem. 267, 2557-2562, 1992
A: Title: The 5'-flanking region of the human calreticulin gene shares homology with the
A: Reference number: A42330; MUID: 92129342; PMID: 1733953
A: Accession: A42330
A: Molecule type: DNA
A: Residues: 1-417 <MC2>
A: Note: sequence extracted from NCBI backbone (NCBIN: 78537, NCBI: 78536)
R: McCauliffe, D.P.; Lux, F.A.; Lieu, T.S.; Sanz, I.; Hanke, J.; Newkirk, M.M.; Bachinski
J. Clin. Invest. 85, 1379-1391, 1990
A: Title: Molecular cloning, expression, and chromosome 19 localization of a human Ro/SS-
A: Reference number: A37047; MUID: 90237213; PMID: 2332496
A: Accession: A37047
A: Molecule type: mRNA
A: Residues: 1-417 <MCC>
A: Cross-references: GB: M32294; NID: G337486; PIDN: AAA36582.1; PID: G337487
A: Note: the authors translated the codon GTA for residue 349 as Tyr
R: Rokeach, L.A.; Haselby, J.A.; Meilof, J.F.; Smeenk, R.J.; Unnasch, T.R.; Greene, B.M.;
J. Immunol. 147, 3031-3039, 1991
A: Title: Characterization of the autoantigen calreticulin.
A: Reference number: A46452; MUID: 92013129; PMID: 1919005
A: Accession: A46452
A: Molecule type: mRNA
A: Residues: 1-417 <KOK>
A: Cross-references: GB: M84739; NID: G179881; PIDN: AAA51916.1; PID: G179882
A: Note: sequence extracted from NCBI backbone (NCBIN: 60749, NCBI: 60750)
R: Lieu, T.S.; Newkirk, M.M.; Capra, J.D.; Sontheimer, R.D.
J. Clin. Invest. 82, 96-101, 1988
A: Title: Molecular characterization of human Ro/SS-A antigen. Amino terminal sequence of
A: Reference number: A28812; MUID: 88273610; PMID: 3260607
A: Accession: A28812
A: Molecule type: protein
A: Residues: 18-41 <LIE>
A: Note: 18-Ala was also found
R: Dupuis, M.; Schaefer, E.; Krause, K.H.; Tschopp, J.
J. Exp. Med. 177, 1-7, 1993
A: Title: The calcium-binding protein calreticulin is a major constituent of lytic granul
A: Reference number: PH1525; MUID: 93115648; PMID: 8418194
A: Accession: PH1525
A: Molecule type: protein
A: Residues: 18-27 <DUP>
A: Experimental source: LAK cell
R: Rojiani, M.V.; Finlay, B.B.; Gray, V.; Dedhar, S.
Biochemistry 30, 9859-9866, 1991
A: Title: In vitro interaction of a polypeptide homologous to human Ro/SS-A antigen (calr
A: Reference number: A40346; MUID: 92002034; PMID: 1911778
A: Accession: A40346

A:Molecule type: protein
A:Residues: 18-34, 'R' <RQ>
R:Krause, K.H.; Simmerman, H.K.B.; Jones, L.R.; Campbell, K.P.
Biochem. J. 270, 545-548, 1990
A:Title: Sequence similarity of calreticulin with a Ca(2+)-binding protein that co-purifies with the ER
A:Reference number: S11475; MUID:90380058; PMID:2400400
A:Accession: S11475
A:Molecule type: protein
A:Residues: 18-32 <KRA>
R:Lamerdin, J.; McCreedy, P.; Stillwagen, S.; Ramirez, M.; Carrano, A.
Submitted to the EMBL Data Library, November 1996
A:Description: Characterization by genomic sequence analysis of a gene-rich 111 kb region on human chromosome 12p13.3
A:Reference number: Z22906
A:Accession: T45075
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-417 <LAM>
A:Cross-references: EMBL:AD000092; PIDN:AA851176.1
A:Experimental source: cell line 5HL2-B; fibroblast
C:Comment: Autoantibodies specific for this protein are found in Sjogren's syndrome and other autoimmune diseases
C:Genetics:
A:Gene: GDB:CALR
A:Cross-references: GDB:125179; OMIM:109091
A:Map position: 19p13.3-19p13.2
A:Introns: 31/1; 65/1; 133/1; 164/3; 234/3; 272/3; 320/3; 351/3
A:Note: CRTC
C:Superfamily: calreticulin
C:Keywords: calcium binding; integrin binding
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-417/Product: calreticulin #status predicted <MAT>
F:414-417/Region: endoplasmic reticulum retention signal
Query Match 100.0%; Score 318; DB 1; Length 417;
Best Local Similarity 100.0%; Pred. No. 6.3e-30;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 138 GPGTKKVVHVFNYGKGNVLINKDIRCKDDEFTHTLTVLRPDNTYEVKIDNSQVSGSLE 197
1 GPGTKKVVHVFNYGKGNVLINKDIRCKDDEFTHTLTVLRPDNTYEVKIDNSQVSGSLE 60
138 GPGTKKVVHVFNYGKGNVLINKDIRCKDDEFTHTLTVLRPDNTYEVKIDNSQVSGSLE 197

RESULT 4

A34154
calreticulin precursor, skeletal muscle - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A34154; S13047
R:Fliegel, L.; Burns, K.; MacLennan, D.H.; Reithmeier, R.A.F.; Michalak, M.
J. Biol. Chem. 264, 21522-21528, 1989
A:Title: Molecular cloning of the high affinity calcium-binding protein (calreticulin) cDNA from rabbit skeletal muscle
A:Reference number: A34154; MUID:90094320; PMID:2600080
A:Accession: A34154
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-418 <FLI>
A:Cross-references: GB:J05138; NID:9164858; PIDN:AA31188.1; PID:9164859
R:Treves, S.; de Mattei, M.; Lanfredi, M.; Villa, A.; Green, N.M.; MacLennan, D.H.; Meldolesi, J. 271, 473-480, 1990
Biochem. J. 271, 473-480, 1990
A:Title: Calreticulin is a candidate for a caldesmon-like function in Ca(2+)-storage
A:Reference number: S13045; MUID:91054414; PMID:2241926
A:Accession: S13047
A:Molecule type: protein
A:Residues: 19-32 <RRE>
C:Superfamily: calreticulin
C:Keywords: skeletal muscle
F:1-17/Domain: signal sequence #status predicted <SIG>
F:415-418/Region: endoplasmic reticulum retention signal

Query Match 100.0%; Score 318; DB 1; Length 418;
Best Local Similarity 100.0%; Pred. No. 6.3e-30;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPGTKKVVHVFNYGKGNVLINKDIRCKDDEFTHTLTVLRPDNTYEVKIDNSQVSGSLE 60

DB 138 GPGTKKVVHVFNYGKGNVLINKDIRCKDDEFTHTLTVLRPDNTYEVKIDNSQVSGSLE 197
RESULT 5
S3376
calreticulin, brain isoform 1 - bovine
C:Species: Bos primigenius taurus (cattle)
C>Date: 20-Oct-1994 #sequence_revision 23-Mar-1995 #text_change 07-May-1999
C:Accession: S43376; S36801
R:Matsuoka, K.; Seta, K.; Yamakawa, Y.; Okuyama, T.; Shinoda, T.; Isobe, T.
Biochem. J. 298, 435-442, 1994
A:Title: Covalent structure of bovine brain calreticulin.
A:Reference number: S43376; MUID:94183174; PMID:8135753
A:Accession: S43376
A:Molecule type: protein
A:Residues: 1-400 <MAT>
A:Experimental source: brain
R:Liu, N.; Pine, R.E.; Johnson, R.J.
Biochim. Biophys. Acta 1202, 70-76, 1993
A:Title: Comparison of cDNAs from bovine brain coding for two isoforms of calreticulin.
A:Reference number: S36799; MUID:93385184; PMID:8373827
A:Accession: S36801
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 45-63, 'E', '65-83 <LIU>
A:Experimental source: brain, clone 8.1
C:Superfamily: calreticulin
C:Keywords: calcium binding; glycoprotein
F:197-400/Region: endoplasmic reticulum retention signal
F:120-146/Disulfide bonds: #status experimental
F:162/Binding site: carbohydrate (Asn) (covalent) #status experimental
Query Match 98.4%; Score 313; DB 2; Length 400;
Best Local Similarity 98.3%; Pred. No. 2.3e-29;
Matches 59; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 GPGTKKVVHVFNYGKGNVLINKDIRCKDDEFTHTLTVLRPDNTYEVKIDNSQVSGSLE 60
121 GPGTKKVVHVFNYGKGNVLINKDIRCKDDEFTHTLTVLRPDNTYEVKIDNSQVSGSLE 180
RESULT 6
S36799
calreticulin precursor, brain isoform 2 - bovine
C:Species: Bos primigenius taurus (cattle)
C>Date: 10-Dec-1993 #sequence_revision 23-Mar-1995 #text_change 13-Aug-1999
C:Accession: S36799; S36800
R:Liu, N.; Pine, R.E.; Johnson, R.J.
Biochim. Biophys. Acta 1202, 70-76, 1993
A:Title: Comparison of cDNAs from bovine brain coding for two isoforms of calreticulin.
A:Reference number: S36799; MUID:93385184; PMID:8373827
A:Accession: S36799
A:Molecule type: mRNA
A:Residues: 1-421 <LIU>
A:Cross-references: GB:LI3462; NID:9348693; PIDN:AAC37307.1; PID:9348694
A:Experimental source: brain, clone 9.4
A:Accession: S36800
A:Molecule type: protein
A:Residues: 35-45 <LI2>
C:Superfamily: calreticulin
C:Keywords: calcium binding; glycoprotein
F:1-34/Domain: signal sequence #status predicted <SIG>
F:35-421/Product: calreticulin, brain isoform 2 #status predicted <MAT>
F:418-421/Region: endoplasmic reticulum retention signal
F:141-167/Disulfide bonds: #status predicted
F:183/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 98.4%; Score 313; DB 2; Length 421;
Best Local Similarity 98.3%; Pred. No. 2.5e-29;
Matches 59; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPGTKKVVHVFNYGKGNVLINKDIRCKDDEFTHTLTVLRPDNTYEVKIDNSQVSGSLE 60

Db 142 GPGTKKHVIFNYKGNVLINKDIRCKDDFTLTLVIRPNTYEVKIDNSQVSGSLE 201
|||||
calreticulin precursor - California sea hare
N:Alternate names: Protein 407
C:Species: Aplysia californica (California sea hare)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: JH0795; F60977
R:Kennedy, T.E.; Kuhl, D.; Barzilai, A.; Sweatt, J.D.; Kandel, E.R.
Neuron 9, 1013-1024, 1992
A:Title: Long-term sensitization training in aplysia leads to an increase in calreticulin
A:Reference number: JH0795; PMID:93098937; PMID:1463604
A:Accession: JH0795
A:Molecule type: mRNA
A:Residues: 1-405 <KEN>
A:Cross-references: GB:551239; NID:G262053; PIDN:BA24569.1; PID:G262054
A:Experimental source: abdominal ganglion and antral nervous system
R:Kennedy, T.E.; Gawinowicz, M.A.; Barzilai, A.; Kandel, E.R.; Sweatt, J.D.
Proc. Natl. Acad. Sci. U.S.A. 85, 7008-7012, 1988
A:Title: Sequencing of proteins from two-dimensional gels by using in situ digestion and
tion in Aplysia.
A:Reference number: A94207; PMID:88320566; PMID:3413132
A:Accession: B31409
A:Molecule type: protein
A:Residues: 'X', 17-28, 'X', 30-31 <KE2>
R:Sweatt, J.D.; Kennedy, T.E.; Wager-Smith, K.; Gawinowicz, M.A.; Barzilai, A.; Karl, K.
Electrophoresis 10, 152-157, 1989
A:Title: Development of a database of amino acid sequences for proteins identified and i
A:Reference number: A60977; PMID:89276264; PMID:2731514
A:Accession: F60977
A:Molecule type: protein
A:Residues: 'X', 17-28, 'X', 30-31 <SWE>
C:Superfamily: calreticulin
C:Keywords: calcium binding; endoplasmic reticulum
F:1-15/Domain: signal sequence #status predicted <SIG>
F:16-405/Product: calreticulin #status experimental <MAT>
F:402-405/Region: endoplasmic reticulum retention signal

Query Match 88.4%; Score 281; DB 1; Length 405;
Best Local Similarity 85.0%; Pred. No. 1.5e-25;
Matches 51; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 GPGTKKHVIFNYKGNVLINKDIRCKDDFTLTLVIRPNTYEVKIDNSQVSGSLE 60
|||||
Db 134 GPGTKKHVIFNYKGNVLINKDIRCKDDFTLTLVIRPNTYEVKIDNEKESGDL 193
|||||

RESULT 8
S29130
calreticulin (clone 8) - African clawed frog (fragment)
C:Species: Xenopus laevis (African clawed frog)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
C:Accession: S29130; T01068
R:Traves, S.; Zorzato, F.; Pozzan, T.
Biochem. J. 287, 579-581, 1992
A:Title: Identification of calreticulin isoforms in the central nervous system.
A:Reference number: S29129; PMID:93074997; PMID:1445218
A:Accession: S29130
A:Molecule type: mRNA
A:Residues: 1-384 <TRF>
A:Cross-references: EMBL:X67598
A:Status: preliminary
A:Accession: T01068
A:Molecule type: mRNA
A:Residues: 1-339, 'XTGR', <TRF>
A:Cross-references: EMBL:X67598; NID:G64610; PIDN:CAA47867.1; PID:G64611
A:Experimental source: CNS
C:Superfamily: calreticulin
C:Keywords: glycoprotein
F:381-384/Region: endoplasmic reticulum retention signal

F:316/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 87.4%; Score 278; DB 2; Length 384;
Best Local Similarity 88.3%; Pred. No. 3.2e-25;
Matches 53; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 GPGTKKHVIFNYKGNVLINKDIRCKDDFTLTLVIRPNTYEVKIDNSQVSGSLE 60
|||||
Db 110 GPGTKKHVIFNYKGNVLINKDIRCKDDFTLTLVIRPNTYEVKIDNSQVSGSLE 169
|||||

RESULT 9
S29129
calreticulin precursor (clone 3) - African clawed frog (fragment)
C:Species: Xenopus laevis (African clawed frog)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
C:Accession: S29129
R:Traves, S.; Zorzato, F.; Pozzan, T.
Biochem. J. 287, 579-581, 1992
A:Title: Identification of calreticulin isoforms in the central nervous system.
A:Reference number: S29129; PMID:93074997; PMID:1445218
A:Accession: S29129
A:Molecule type: mRNA
A:Residues: 1-411 <TRF>
A:Cross-references: EMBL:X67597; NID:G64608; PIDN:CAA47866.1; PID:G64609
C:Superfamily: calreticulin
C:Keywords: glycoprotein
F:1-12/Domain: signal sequence (fragment) #status predicted <SIG>
F:13-411/Product: calreticulin #status predicted <MAT>
F:408-411/Region: endoplasmic reticulum retention signal
F:339/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 87.4%; Score 278; DB 2; Length 411;
Best Local Similarity 88.3%; Pred. No. 3.4e-25;
Matches 53; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 GPGTKKHVIFNYKGNVLINKDIRCKDDFTLTLVIRPNTYEVKIDNSQVSGSLE 60
|||||
Db 133 GPGTKKHVIFNYKGNVLINKDIRCKDDFTLTLVIRPNTYEVKIDNSQVSGSLE 192
|||||

RESULT 10
A56637
calreticulin homolog precursor - fruit fly (Drosophila melanogaster)
N:Alternate names: Ro/SS-A autoantigen/calreticulin homolog
C:Species: Drosophila melanogaster
C>Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 13-Aug-1999
C:Accession: A56637; A37158
R:Smith, M.J.
DNA Seq. 3, 247-250, 1992
A:Title: Nucleotide sequence of a Drosophila melanogaster gene encoding a calreticulin h
A:Reference number: A56637; PMID:93208374; PMID:1296819
A:Accession: A56637
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-406 <SMI>
A:Cross-references: GB:X64461; NID:G7685; PIDN:CAA45791.1; PID:G7686
A:Note: sequence extracted from NCBI backbone (NCBI:128274, NCBI:128275)
R:McCaulliffe, D.P.; Zappi, E.; Lieu, T.S.; Michalak, M.; Sontheimer, R.D.; Capra, J.D.
J. Clin. Invest. 86, 332-335, 1990
A:Title: A human Ro/SS-A autoantigen is the homologue of calreticulin and is highly homo
A:Reference number: A37158; PMID:90307981; PMID:1236582
A:Accession: A37158
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 91-105, 'A', 107, 109-124, 182-183, 'L', 185-220 <MCC>
C:Genetics:
A:Gene: FlyBase:Crc
A:Cross-references: FlyBase:FBgn0005585
A:Introns: 65/1; 22/3
C:Superfamily: calreticulin
C:Keywords: calcium binding; endoplasmic reticulum
F:1-17/Domain: signal sequence #status predicted <SIG>

F:403-406/Region: endoplasmic reticulum retention signal

Query Match 84.6%; Score 269; DB 2; Length 406;
Best Local Similarity 83.3%; Pred. No. 3.9e-24;
Matches 50; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 GPGTKKVVHVFYNYKGNVINKDKDETHLYTLVIRPDNTYEVKIDNSQVSGSLE 60
|||||
DB 138 GPGTKKVVHVFYNYKGNVINKDKDETHLYTLVIRPDNTYEVKIDNSQVSGSLE 197
|||||

RESULT 11

S71343
calreticulin precursor - Korean frog
C:Species: Rana rugosa (Korean frog)
C:Date: 29-Jan-1998 #sequence_revision 13-Feb-1998 #text_change 20-Jun-2000
C:Accession: S71343
R:Yamamoto, S.; Nakamura, M.
FEBS Lett. 387, 27-32, 1996
A:Title: Calnexin: its molecular cloning and expression in the liver of the frog, Rana
A:Reference number: S71342; MUID:96234004; PMID:8654561
A:Accession: S71343
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-419 <YAM>
A:Cross-references: EMBL:D78589; NID:gl514956; PIDN:BAAL1425.1; PID:gl514957
C:Keywords: calcium binding; endoplasmic reticulum
C:Superfamily: calreticulin
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-419/Product: calreticulin #status predicted <MAT>
F:205-213/Region: nuclear location signal
F:415-418/Region: endoplasmic reticulum retention signal

Query Match 82.4%; Score 262; DB 2; Length 419;
Best Local Similarity 83.3%; Pred. No. 2.8e-23;
Matches 50; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 GPGTKKVVHVFYNYKGNVINKDKDETHLYTLVIRPDNTYEVKIDNSQVSGSLE 60
|||||
DB 139 GPGTKKVVHVFYNYKGNVINKDKDETHLYTLVIRPDNTYEVKIDNSQVSGSLE 198
|||||

RESULT 12

A32507
41k larval antigen - nematode (Onchocerca volvulus) (fragment)
C:Species: Onchocerca volvulus
C:Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 12-Apr-1995
C:Accession: A32507; A28813
R:Unasch, T.R.; Gallin, M.Y.; Soboslay, P.T.; Ertmann, K.D.; Greene, B.M.
J. Clin. Invest. 82, 262-269, 1988
A:Title: Isolation and characterization of expression cDNA clones encoding antigens of
A:Reference number: A92769; MUID:88273584; PMID:2455736
A:Accession: A32507
A:Molecule type: mRNA
A:Residues: 1-336 <UNN>
C:Superfamily: calreticulin

Query Match 76.1%; Score 242; DB 2; Length 336;
Best Local Similarity 75.0%; Pred. No. 5.1e-21;
Matches 45; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 1 GPGTKKVVHVFYNYKGNVINKDKDETHLYTLVIRPDNTYEVKIDNSQVSGSLE 60
|||||
DB 84 GPGTKKVVHVFYNYKGNVINKDKDETHLYTLVIRPDNTYEVKIDNSQVSGSLE 143
|||||

RESULT 13

A48573
calreticulin autoantigen homolog precursor - fluke (Schistosoma mansoni)
C:Species: Schistosoma mansoni
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A48573
R:Khailaie, J.; Proteine, F.; Schacht, A.M.; Godin, C.; Pierce, R.J.; Capron, A.

Mol. Biochem. Parasitol. 57, 193-202, 1993
A:Title: Cloning of the gene encoding a Schistosoma mansoni antigen homologous to human
A:Reference number: A48573; MUID:93165070; PMID:8433712
A:Accession: A48573
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-393 <KHA>
A:Cross-references: GB:M93097; NID:gl60928
A:Note: sequence inconsistent with the nucleotide translation
A:Note: sequence extracted from NCBI backbone (NCBIN:125085, NCBIP:125086)
C:Superfamily: calreticulin
F:1-16/Domain: signal sequence #status predicted <SIG>
F:390-393/Region: endoplasmic reticulum retention signal

Query Match 71.4%; Score 227; DB 1; Length 393;
Best Local Similarity 73.3%; Pred. No. 3.6e-19;
Matches 44; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 1 GPGTKKVVHVFYNYKGNVINKDKDETHLYTLVIRPDNTYEVKIDNSQVSGSLE 60
|||||
DB 136 GPGTKKVVHVFYNYKGNVINKDKDETHLYTLVIRPDNTYEVKIDNSQVSGSLE 195
|||||

RESULT 14

S25851
calreticulin precursor - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 06-Jan-1994 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999
C:Accession: S25851; T33996
R:Smith, M.J.
DNA Seq. 2, 235-240, 1992
A:Title: A. C. elegans gene encodes a protein homologous to mammalian calreticulin.
A:Reference number: S25851; MUID:92329978; PMID:1627827
A:Accession: S25851
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-395 <SMI>
A:Cross-references: EMBL:X59589; NID:g6693; PIDN:CAA42159.1; PID:g6694
R:Bauer, C.; Courtney, L.; Laplant, Y.
submitted to the EMBL Data Library, February 1999
A:Description: The sequence of C. elegans cosmid Y38A10A.
A:Reference number: Z21453
A:Accession: T33996
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-395 <BAU>
A:Cross-references: EMBL:AF125963; PIDN:AAD14746.1; GSPDB:GN000023; CESP:Y38A10A.5
A:Experimental source: strain Bristol N2; clone Y38A10A
C:Genetics:
A:Gene: CESP:Y38A10A.5
A:Map position: 5
A:Introns: 107/3; 315/3
C:Superfamily: calreticulin
F:1-15/Domain: signal sequence #status predicted <SIG>
F:392-395/Region: endoplasmic reticulum retention signal

Query Match 66.2%; Score 210.5; DB 2; Length 395;
Best Local Similarity 66.7%; Pred. No. 3.3e-17;
Matches 40; Conservative 7; Mismatches 12; Indels 1; Gaps 1;

QY 1 GPGTKKVVHVFYNYKGNVINKDKDETHLYTLVIRPDNTYEVKIDNSQVSGSLE 60
|||||
DB 134 GP-TRRVHVLVNYKGNVINKDKDETHLYTLVIRPDNTYEVKIDNSQVSGSLE 192
|||||

RESULT 15

T14554
calreticulin - beet
C:Species: Beta vulgaris (beet)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Jun-2000
C:Accession: T14554
R:Vioreck, R.
submitted to the EMBL Data Library, October 1997

A:Description: Nucleotide sequence from sugar beet calreticulin.

A:Reference number: Z18137

A:Accession: T14534

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-416 <VIE>

A:Cross-references: EMBL:AJ002057

A:Experimental source: strain diploide Inzuchtlinie KWS; leaf

C:Superfamily: calreticulin

C:Keywords: calcium binding

Query Match 57.9%; Score 184; DB 2; Length 416;
Best Local Similarity 55.9%; Pred. No. 4.9e-14;
Matches 33; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

QY 1 GPGTKVHVIFNFKGKVLINKDIRCKDDEFTHTLVLPDNTYEVKIDNSQVESGSL 59

DB 144 GYSPKKVHAIFNNDTNHLLIKKDVPCETDQTHVTFILRPDATYSILIDNOEKQTGSL 202

Search completed: October 4, 2004, 13:06:35
Job time : 13.0588 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 4, 2004, 12:52:12 ; Search time 8.82353 Seconds
(without alignments)
354.077 Million cell updates/sec

Title: US-09-807-148-8

Perfect score: 318

Sequence: 1 GPCTKKVHFVFNKGNVLI.....PDNTVEVKIDNSQVSGSLE 60

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	318	100.0	416	1	CRTC MOUSE
2	318	100.0	416	1	CRTC RAT
3	318	100.0	417	1	CRTC CRIGR
4	318	100.0	417	1	CRTC HUMAN
5	318	100.0	418	1	CRTC RABIT
6	318	98.4	417	1	CRT1 BOVIN
7	313	98.4	421	1	CRT2 BOVIN
8	269	84.6	406	1	CRTC DROME
9	242	76.1	388	1	RALI ONCVO
10	227	71.4	393	1	CRTC SCHWA
11	210.5	66.2	395	1	CRTC CAEEL
12	199	62.6	420	1	CRTC CHLRE
13	184	57.9	416	1	CRTC BETVU
14	179	56.3	421	1	CRTC PRUAR
15	177.5	55.8	424	1	CRTC DICDI
16	177	55.7	415	1	CRTC RICCO
17	177	55.7	424	1	CRTC ARATH
18	175	55.0	384	1	CRT3 HUMAN
19	173	54.4	380	1	CRT1 MOUSE
20	172	54.1	425	1	CRT1 ARATH
21	171	53.8	424	1	CRTC ORYSA
22	170	53.5	420	1	CRTC MAIZE
23	169	53.1	416	1	CRTC NICPL
24	166	52.2	401	1	CRTC EUGER
25	166	52.2	424	1	CRT3 ARATH
26	154	48.4	416	1	CRTC BERST
27	117	36.8	592	1	CALX HUMAN
28	116	36.5	591	1	CALX MOUSE
29	116	36.5	591	1	CALX RAT
30	115	36.2	593	1	CALX CANFA
31	107	33.6	610	1	CALG HUMAN
32	106	33.3	611	1	CALG MOUSE
33	98	30.8	619	1	CALX CAEEL

34	97.5	30.7	560	1	CALX SCHPO
35	87	27.4	546	1	CALX SOYBN
36	82	25.8	530	1	CAX1 ARATH
37	77	24.2	540	1	CALX HELTU
38	77	24.2	551	1	CALX PEA
39	72	22.6	532	1	CAX2 ARATH
40	64.5	20.3	540	1	XTAL ACICA
41	61.5	19.3	582	1	SYN2 HUMAN
42	61	19.2	474	1	LAM3 MOUSE
43	61	19.2	592	1	LAM2 MOUSE
44	60.5	19.0	586	1	SYN2 RAT
45	59.5	18.7	220	1	PSD9 YEAST

ALIGNMENTS

RESULT 1	CRTC_MOUSE	STANDARD;	PRT;	416 AA.
ID	CRTC_MOUSE	STANDARD;	PRT;	416 AA.
AC	P14211;			
DT	01-JAN-1990 (Rel. 13, Created)			
DT	01-JAN-1990 (Rel. 13, Last sequence update)			
DT	15-MAR-2004 (Rel. 43, Last annotation update)			
DE	Calreticulin precursor (CRP55) (Calregulin) (HACBP) (ERP60).			
GN	CALR.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A. AND SEQUENCE OF 18-48 AND 129-161.			
RP	STRAIN-BALB/C; TISSUE=Liver;			
RX	MEDLINE=90059955; PubMed=2583110;			
RA	Smith M.J., Koch G.L.E.;			
RT	"Multiple zones in the sequence of calreticulin (CRP55, calregulin,			
RT	HACBP), a major calcium binding ER/SR protein.";			
RL	EMBO J. 8:3581-3586(1989).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RP	MEDLINE=93013037; PubMed=1398135;			
RA	Mazzarella R.A., Gold P., Cunningham M., Green M.;			
RT	"Determination of the sequence of an expressible cDNA clone encoding			
RT	ERP60/calregulin by the use of a novel nested set method.";			
RL	Gene 120:217-225(1992).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RP	STRAIN=FVB/N-3; TISSUE=Mammary gland;			
RP	MEDLINE=22388257; PubMed=12477932;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,			
RA	Klausner R.D., Collins F.S., Wagner K.H., Schaefer C.F., Bhat N.K.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Wang J., Wang J., Hsieh F.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,			
RA	Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hsieh T.E.,			
RA	Stapleton M., Scars M.B., Donald M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Sherchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Tuchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Gricham J.J., Schmutz J., Myers R.M.,			
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,			
RA	Schneerch A., Schein J.E., Jones S.J.M., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length			
RT	human and mouse cDNA sequences";			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
RN	[4]			
RP	SEQUENCE OF 18-38.			
RP	TISSUE=Fibroblast;			
RP	MEDLINE=95009907; PubMed=7523108;			

RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
 RT "Separation and sequencing of familial and novel murine proteins
 RL using preparative two-dimensional gel electrophoresis.";
 CC Electrophoresis 15:735-745(1994).
 CC -!- FUNCTION: This protein binds calcium. There are both high and
 CC low affinity calcium-binding sites.
 CC -!- SUBUNIT: Monomer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
 CC -!- SIMILARITY: Belongs to the calreticulin family.

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 CC or send an email to license@isb-sib.ch).

CC -----
 CC EMBL; X14326; CAA33053.1; -;
 DR EMBL; M52988; AAA37569.1; -;
 DR EMBL; BC003453; AAA03453.1; -;
 DR PIR; S06763; S06763.
 DR SWISS-2DPAGE; P14211; MOUSE.
 DR MGD; MGI:88252; Calr.
 DR GO; GO:0005509; F:calcium ion binding; IDA.
 DR InterPro; IPR009033; Calreticalex_P.
 DR InterPro; IPR001580; Calreticulin.
 DR InterPro; IPR009985; ConA_like_rec_gl.
 DR Pfam; PF00262; calreticulin; 1.
 DR PIRSF; PIRSF002356; Calreticulin; 1.
 DR PRINTS; P00626; CALRETICULIN.
 DR ProDom; PD01866; Calreticulin; 1.
 DR PROSITE; PS00014; ER TARGET; 1.
 DR PROSITE; PS00803; CALRETICULIN_1; 1.
 DR PROSITE; PS00804; CALRETICULIN_2; 1.
 DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
 FT SIGNAL 1 17
 FT CHAIN 18 416 CALRETICULIN.
 FT DOMAIN 18 197 N-DOMAIN.
 FT DOMAIN 198 208 P-DOMAIN.
 FT DOMAIN 309 416 C-DOMAIN.
 FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.
 FT REPEAT 191 202 1-1.
 FT REPEAT 210 221 1-2.
 FT REPEAT 227 238 1-3.
 FT REPEAT 244 255 1-4.
 FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.
 FT REPEAT 259 269 2-1.
 FT REPEAT 273 283 2-2.
 FT REPEAT 287 297 2-3.
 FT DOMAIN 351 407 ASP/GLU/LYS-RICH.
 FT DISULFID 137 163 BY SIMILARITY.
 FT SITE 413 416 PREVENT SECRETION FROM ER.
 SQ SEQUENCE 416 AA; 47994 MW; 24C03B00913408D8 CRC64;

Query Match 100.0%; Score 318; DB 1; Length 416;
 Best Local Similarity 100.0%; Pred. No. 1.le-31;
 Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPGTKKHVINYKGNVLINKIRCKDDFTHTLYLIVRPDNTYEVKIDNSQVSGSLE 60
 Db 138 GPGTKKHVINYKGNVLINKIRCKDDFTHTLYLIVRPDNTYEVKIDNSQVSGSLE 197

RESULT 2

CRTC_RAT STANDARD; PRT; 416 AA.
 ID CRTC_RAT
 AC P18418; P10452;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Calreticulin precursor (CRP55) (Calregulin) (HACBP) (ERP60) (CALBP)
 DE (Calcium-binding protein 3) (CABP3).
 GN CALR.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Brain cortex;
 RX MEDLINE=90370496; PubMed=2395661;
 RA Murthy K.K., Banville D., Srikant C.B., Carrier F., Bell A.,
 RA Holmes C., Patel Y.C.;
 RT "Structural homology between the rat calreticulin gene product and
 RT the Onchocerca volvulus antigen Ral-1.";
 RL Nucleic Acids Res. 18:4933-4933(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RX MEDLINE=93202172; PubMed=8453984;
 RA Nakamura M., Moriya M., Baba T., Michikawa Y., Yamanobe T., Arai K.,
 RA Okinaga S., Kobayashi T.;
 RT "An endoplasmic reticulum protein, calreticulin, is transported into
 RT the acrosome of rat sperm.";
 RL Exp. Cell Res. 205:101-110(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Liver;
 RX MEDLINE=95181573; PubMed=7876339;
 RA Soennichsen B., Fueflekrug J., van Nguyen P., Diekmann W.,
 RA Robinson D.G., Mieskes G.;
 RT "Retention and retrieval: both mechanisms cooperate to maintain
 RT calreticulin in the endoplasmic reticulum.";
 RL J. Cell Sci. 107:2705-2717(1994).
 RN [4]
 RP SEQUENCE OF 270-359 FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RX Lone Y.C., Bailly A., Latruffe N.;
 RA Submitted (DEC-1988) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 18-29.
 RX MEDLINE=91054414; PubMed=2241926;
 RA Traves S., de Mattei M., Lanfredi M., Villa A., Green N.M.,
 RA MacLennan D.H., Meldolesi J., Pozzan T.;
 RT "Calreticulin is a candidate for a calsequestrin-like function in
 RT Ca2(+)-storage compartments (calciosomes) of liver and brain.";
 RL Biochem. J. 271:473-480(1990).
 RN [6]
 RP SEQUENCE OF 18-32.
 RC STRAIN=Sprague-Dawley; TISSUE=Testis;
 RX MEDLINE=92360010; PubMed=1497655;
 RA Nakamura M., Michikawa Y., Baba T., Okinaga S., Arai K.;
 RT "Calreticulin is present in the acrosome of spermatids of rat
 RT testis.";
 RL Biochem. Biophys. Res. Commun. 186:668-673(1992).
 RN [7]
 RP SEQUENCE OF 18-32.
 RC STRAIN=LSC; TISSUE=Liver;
 RX MEDLINE=94072621; PubMed=8251535;
 RA Yokoi T., Nagayama S., Kajiura R., Kawaguchi Y., Horiuchi R.,
 RA Kamataki T.;
 RT "Identification of protein disulfide isomerase and calreticulin as
 RT autoantigen antigens in LSC strain of rats.";
 RL Biochim. Biophys. Acta 1158:339-344(1993).
 CC -!- FUNCTION: This protein binds calcium. There are both high and low
 CC affinity calcium-binding sites.
 CC -!- SUBUNIT: Monomer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
 CC -!- SIMILARITY: Belongs to the calreticulin family.
 CC -!- CAUTION: Was originally (Ref.2) thought to be D-beta-
 CC hydroxybutyrate dehydrogenase.
 CC -----
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Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
-!- FUNCTION: This protein binds calcium. There are both high and low affinity calcium-binding sites.
-!- SUBUNIT: Monomer.
-!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
-!- SIMILARITY: Belongs to the calreticulin family.

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EMBL; AY100688; AAM48568.1; InterPro; IPR009033; Calret calnex_P. InterPro; IPR001580; Calreticulin. InterPro; IPR008985; ConA like lec_gl. InterPro; IPR008886; ER_target_S. Pfam; PF00262; calreticulin; 1. PRINTS; PIRSF002356; Calreticulin; 1. PROSITE; PS001866; Calreticulin; 1. PROSITE; PS00803; CALRETICULIN_1; 1. PROSITE; PS00804; CALRETICULIN_2; 1. PROSITE; PS00805; CALRETICULIN_REPEAT; 3. PROSITE; PS00014; ER_TARGET; 1. Endoplasmic reticulum; Calcium-binding; Repeat; Glycoprotein; Signal.
KW SIGNAL 1 17
FT CHAIN 18 417 CALRETICULIN.
FT DOMAIN 18 197 N-DOMAIN.
FT DOMAIN 198 308 P-DOMAIN.
FT DOMAIN 309 417 C-DOMAIN.
FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.
FT REPEAT 191 202 1-1.
FT REPEAT 210 221 1-2.
FT REPEAT 227 238 1-3.
FT REPEAT 244 255 1-4.
FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.
FT REPEAT 259 269 2-1.
FT REPEAT 273 283 2-2.
FT REPEAT 287 297 2-3.
FT DOMAIN 351 407 ASP/GLU/LYS-RICH.
FT DISULFID 137 163 BY SIMILARITY.
FT SITE 413 416 PREVENT SECRETION FROM ER.
FT SITE 414 417 PREVENT SECRETION FROM ER (POTENTIAL).
SQ SEQUENCE 417 AA; 48242 MW; D617DA37D14F2D45 CRC64;

Query Match 100.0%; Score 318; DB 1; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.1e-31;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPGTKKHVIFNYKGNVLINKDKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSLE 60
DB 138 GPGTKKHVIFNYKGNVLINKDKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSLE 197

RESULT 4
ID CRTG_HUMAN STANDARD; PRT; 417 AA.
AC P27797;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Calreticulin precursor (CRP55) (Calregulin) (HACBP) (ERP60).
GN CALR OR CRTG
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
OX [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=92013129; PubMed=1919005;
RX

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EMBL; D78308; BAA11345.1; InterPro; IPR009033; Calret calnex_P. EMBL; X53363; CAA37446.1; InterPro; IPR001580; Calreticulin. EMBL; X13702; CAA31987.1; ALT_SEQ. EMBL; X79327; CAA55890.1; InterPro; IPR008985; ConA like lec_gl. FIR; JH0819; JH0819. PDB; 1K91; 12-OCT-02. PDB; 1K9C; 12-OCT-02.
InterPro; IPR009033; Calret calnex_P. InterPro; IPR001580; Calreticulin. InterPro; IPR008985; ConA like lec_gl. InterPro; IPR008886; ER_target_S. Pfam; PF00262; calreticulin; 1. PRINTS; PIRSF002356; Calreticulin; 1. PROSITE; PS001866; Calreticulin; 1. PROSITE; PS00014; ER_TARGET; 1. PROSITE; PS00803; CALRETICULIN_1; 1. PROSITE; PS00804; CALRETICULIN_2; 1. PROSITE; PS00805; CALRETICULIN_REPEAT; 3. Endoplasmic reticulum; Calcium-binding; Repeat; Signal; 3D-structure.
KW SIGNAL 1 17
FT CHAIN 18 416 CALRETICULIN.
FT DOMAIN 18 197 N-DOMAIN.
FT DOMAIN 198 308 P-DOMAIN.
FT DOMAIN 309 416 C-DOMAIN.
FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.
FT REPEAT 191 202 1-1.
FT REPEAT 210 221 1-2.
FT REPEAT 227 238 1-3.
FT REPEAT 244 255 1-4.
FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.
FT REPEAT 259 269 2-1.
FT REPEAT 273 283 2-2.
FT REPEAT 287 297 2-3.
FT DOMAIN 351 407 ASP/GLU/LYS-RICH.
FT DISULFID 137 163 BY SIMILARITY.
FT SITE 413 416 PREVENT SECRETION FROM ER.
FT SITE 414 417 PREVENT SECRETION FROM ER (POTENTIAL).
SQ SEQUENCE 416 AA; 47995 MW; 2E6713CED31A2970 CRC64;

Query Match 100.0%; Score 318; DB 1; Length 416;
Best Local Similarity 100.0%; Pred. No. 1.1e-31;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPGTKKHVIFNYKGNVLINKDKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSLE 60
DB 138 GPGTKKHVIFNYKGNVLINKDKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSLE 197

RESULT 3
ID CRTG_CRIGR STANDARD; PRT; 417 AA.
AC Q8X3H7;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Calreticulin precursor (CRP55) (Calregulin) (HACBP) (ERP60).
GN CALR.
OS Cricetus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetus.
OC NCBI_TaxID=10029;
OX [1]
RN SEQUENCE FROM N.A.
RP Chung J.Y.; Lee G.M.;


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FT DOMAIN 18 197 N-DOMAIN.
FT DOMAIN 198 308 P-DOMAIN.
FT DOMAIN 309 417 C-DOMAIN.
FT REPEAT 191 255 4 X APPROXIMATE REPEATS.
FT REPEAT 202 221 1-1.
FT REPEAT 210 221 1-2.
FT REPEAT 227 238 1-3.
FT REPEAT 244 255 1-4.
FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.
FT REPEAT 259 297 2-1.
FT REPEAT 273 297 2-2.
FT REPEAT 287 297 2-3.
FT DOMAIN 351 408 ASP/GLU/LYS-RICH.
FT DISULFID 137 163 BY SIMILARITY.
FT SITE 414 417 PREVENT SECRETION FROM ER.
FT CONFLICT 35 35 MISSING (IN REF 3).
SQ SEQUENCE 417 AA; BC37C3C0F1054FB2 CRC64;

Query Match 100.0%; Score 318; DB 1; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.1e-31;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPGTKKHVIFNYKGNVLINKDKCKDEFTHTLVLPDNTYEVKIDNSQVSGSLE 60
DB 138 GPGTKKHVIFNYKGNVLINKDKCKDEFTHTLVLPDNTYEVKIDNSQVSGSLE 197

RESULT 5
CRTC_RABIT
ID -CRTC_RABIT STANDARD; PRT; 418 AA.
AC P15253;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Calreticulin precursor (CRP55) (Calregulin) (HACBP) (ERP60).
GN CALR.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Slow-twitch skeletal muscle;
RX MEDLINE=90094320; PubMed=2600080;
RA Flegel L., Burns K., MacLennan D.H., Reithmeier R.A.F., Michalak M.;
RT "Molecular cloning of the high affinity calcium-binding protein
(caltreticulin) of skeletal muscle sarcoplasmic reticulum.";
RL J. Biol. Chem. 264:21522-21528(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Fast-twitch skeletal muscle;
RX MEDLINE=91282795; PubMed=2059224;
RA Flegel L., Michalak M.;
RT "Fast-twitch and slow-twitch skeletal muscles express the same
isoform of calreticulin.";
RL Biochem. Biophys. Res. Commun. 177:979-984(1991).
RN [3]
RP SEQUENCE OF 18-36.
RX MEDLINE=91054414; PubMed=2241926;
RA Treves S., de Mattei M., Lanfredi M., Villa A., Green N.M.,
RA MacLennan D.H., Meldolesi J., Pozzan T.;
RT "Calreticulin is a candidate for a calsequestrin-like function in
Ca2(+)-storage compartments (calciosomes) of liver and brain.";
RL Biochem. J. 271:473-480(1990).
RN [4]
RP SEQUENCE OF 18-46.
RX MEDLINE=91201375; PubMed=2016321;
RA Milner R.E., Baksh S., Shemanko C., Carpenter M.R., Smillie L.,
RA Vance J.E., Opas M., Michalak M.;
RT "Calreticulin, and not calsequestrin, is the major calcium binding
protein of smooth muscle sarcoplasmic reticulum and liver endoplasmic
reticulum.";
RL J. Biol. Chem. 266:7155-7165(1991).

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[5]
RN PARTIAL SEQUENCE.
RP TISSUE=Lung;
RC MEDLINE=92002038; PubMed=1911780;
RA Guan S., Fallick A.M., Williams D.E., Cashman J.R.;
RT "Evidence for complex formation between rabbit lung flavin-containing
monooxygenase and calreticulin.";
RL Biochemistry 30:9892-9900(1991).
CC -!- FUNCTION: This protein binds calcium. There are both high and low
affinity calcium-binding sites.
CC -!- SUBUNIT: Monomer (by similarity).
CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -!- SIMILARITY: Belongs to the calreticulin family.
CC
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or send an email to license@isb-sib.ch).
CC
CC EMBL; J05138; AAA31188.1; -
DR PIR; A34154; A34154.
DR PIR; C33208; C33208.
DR PIR; S13046; S13046.
DR InterPro; IPR009033; Calret_calnex_P.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR008985; ConA like lec_gl.
DR InterPro; IPR008886; ER_target_S.
DR Pfam; PF00262; calreticulin_1.
DR PIRSF; PIRSF002956; Calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR PRODOM; PD001866; Calreticulin; 1.
DR PROSITE; PS00014; ER_TARGET; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
FT SIGNAL 1 17
FT CHAIN 18 418 CALRETICULIN.
FT DOMAIN 18 197 N-DOMAIN.
FT DOMAIN 198 308 P-DOMAIN.
FT DOMAIN 309 418 C-DOMAIN.
FT DOMAIN 191 255 4 X APPROXIMATE REPEATS.
FT REPEAT 191 202 1-1.
FT REPEAT 202 221 1-2.
FT REPEAT 227 238 1-3.
FT REPEAT 244 255 1-4.
FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.
FT REPEAT 259 269 2-1.
FT REPEAT 273 283 2-2.
FT REPEAT 287 297 2-3.
FT DOMAIN 351 408 ASP/GLU/LYS-RICH.
FT DISULFID 137 163 BY SIMILARITY.
FT SITE 415 418 PREVENT SECRETION FROM ER.
FT VARIANT 35 35 E -> D.
FT CONFLICT 90 90 P -> T (IN REF. 5).
FT SEQUENCE 418 AA; 48275 MW; B6082B689DC763A6 CRC64;

Query Match 100.0%; Score 318; DB 1; Length 418;
Best Local Similarity 100.0%; Pred. No. 1.1e-31;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPGTKKHVIFNYKGNVLINKDKCKDEFTHTLVLPDNTYEVKIDNSQVSGSLE 60
DB 138 GPGTKKHVIFNYKGNVLINKDKCKDEFTHTLVLPDNTYEVKIDNSQVSGSLE 197

RESULT 6
CRTL_BOVIN
ID -CRTL_BOVIN STANDARD; PRT; 417 AA.
AC P52193; Q8SQ53;

```

DT 01-OCT-1996 (Rel. 34, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Calreticulin, brain isoform 1 precursor (CRP55) (Calregulin) (HACBP).
 GN CALR OR CRT.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RC 01-NOV-1995 (Rel. 32, Created)
 RC 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Calreticulin, brain isoform 2 precursor (CRP55) (Calregulin) (HACBP).
 GN Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RC MEDLINE=94183174; PubMed=8135753;
 RX Matsuoka K., Seta K., Yamakawa Y., Okuyama T., Shinoda T., Isobe T.;
 RA "Hovain M.A., Takawa K., Minakata H., Nakajima T.;
 RT "Bovine brain calreticulin";
 RL Biochem. J. 298:435-442(1994).
 RN [2]
 RP Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 18-417.
 RC TISSUE=Brain;
 RC MEDLINE=94183174; PubMed=8135753;
 RX Matsuoka K., Seta K., Yamakawa Y., Okuyama T., Shinoda T., Isobe T.;
 RA "Hovain M.A., Takawa K., Minakata H., Nakajima T.;
 RT "Bovine brain calreticulin";
 RL Biochem. J. 298:435-442(1994).
 CC -!- FUNCTION: This protein binds calcium. There are both high and low
 CC affinity calcium-binding sites.
 CC -!- SUBUNIT: Monomer.
 CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
 CC -!- SIMILARITY: Belongs to the calreticulin family.
 CC
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 CC
 CC EMBL; AB067697; BAB86913.1; -
 DR InterPro; IPR009033; Calret calnex P.
 DR InterPro; IPR001580; Calreticulin.
 DR InterPro; IPR008985; Cona like lec-gl.
 DR InterPro; IPR008986; ER target-S.
 DR Pfam; PF00262; calreticulin; 1.
 DR PRINTS; PIRSF002356; Calreticulin; 1.
 DR PRINTS; PIRSF002356; Calreticulin; 1.
 DR PRODOM; PD001866; Calreticulin; 1.
 DR PROSITE; PS00014; ER TARGET; 1.
 DR PROSITE; PS00803; CALRETICULIN 1; 1.
 DR PROSITE; PS00804; CALRETICULIN 2; 1.
 DR PROSITE; PS00805; CALRETICULIN REPEAT; 3.
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Glycoprotein; Signal.
 FT SIGNAL 1 17
 FT CHAIN 18 417 CALRETICULIN, BRAIN ISOFORM 1.
 FT DOMAIN 18 197 N-DOMAIN.
 FT DOMAIN 198 308 P-DOMAIN.
 FT DOMAIN 309 417 C-DOMAIN.
 FT DOMAIN 151 255 4 X APPROXIMATE REPEATS.
 FT REPEAT 191 202 1-1.
 FT REPEAT 210 221 1-2.
 FT REPEAT 227 238 1-3.
 FT REPEAT 244 255 1-4.
 FT DOMAIN 259 297 3 X APPROXIMATE REPEATS.
 FT REPEAT 259 269 2-1.
 FT REPEAT 273 283 2-2.
 FT REPEAT 287 297 2-3.
 FT DOMAIN 351 407 ASP/GLU/LYS-RICH.
 FT DISULFID 137 163
 FT CARBOHYD 179 179 N-LINKED (GLCNAC...)
 FT SITE 414 417 PREVENT SECRETION FROM ER (POTENTIAL).
 SQ SEQUENCE 417 AA; 48038 MW; 7BF812C7B5417BE9 CRC64;

Query Match 98.4%; Score 313; DB 1; Length 417;
 Best Local Similarity 98.3%; Pred. No. 4.4e-31;

Matches 59; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GPOTKKVHVFNYKGNVLINKDCKDETHLYTLVIRPNTYEVKIDNSQVESGSL 60
 DB 138 GPOTKKVHVFNYKGNVLINKDCKDETHLYTLVIRPNTYEVKIDNSQVESGSL 197
 RESULT 7
 CRT2 BOVIN
 ID CRT2_BOVIN STANDARD; PRT; 421 AA.
 AC P42918;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Calreticulin, brain isoform 2 precursor (CRP55) (Calregulin) (HACBP).
 GN Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RC MEDLINE=93385184; PubMed=8373827;
 RX Liu N., Fine R.E., Johnson R.J.;
 RA "Comparison of cDNAs from bovine brain coding for two isoforms of
 RT calreticulin";
 RL Biochim. Biophys. Acta 1202:70-76(1993).
 CC -!- FUNCTION: This protein binds calcium. There are both high and low
 CC affinity calcium-binding sites.
 CC -!- SUBUNIT: Monomer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
 CC -!- SIMILARITY: Belongs to the calreticulin family.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; L13462; AAC37307.1; -
 DR PIR; S36799; S36799.
 DR InterPro; IPR009033; Calret calnex P.
 DR InterPro; IPR001580; Calreticulin.
 DR InterPro; IPR008985; Cona like lec-gl.
 DR InterPro; IPR008986; ER target-S-gl.
 DR Pfam; PF00262; calreticulin; 1.
 DR PIRSF; PIRSF002356; Calreticulin; 1.
 DR PRINTS; PIRSF002356; Calreticulin; 1.
 DR PRODOM; PD001866; Calreticulin; 1.
 DR PROSITE; PS00014; ER TARGET; 1.
 DR PROSITE; PS00803; CALRETICULIN 1; 1.
 DR PROSITE; PS00804; CALRETICULIN 2; 1.
 DR PROSITE; PS00805; CALRETICULIN REPEAT; 3.
 KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
 FT SIGNAL 1 34 POTENTIAL.
 FT CHAIN 35 421 CALRETICULIN, BRAIN ISOFORM 2.
 FT DOMAIN 35 201 N-DOMAIN.
 FT DOMAIN 202 312 P-DOMAIN.
 FT DOMAIN 313 421 C-DOMAIN.
 FT DOMAIN 195 259 4 X APPROXIMATE REPEATS.
 FT REPEAT 195 206 1-1.
 FT REPEAT 214 225 1-2.
 FT REPEAT 231 242 1-3.
 FT REPEAT 248 259 1-4.
 FT DOMAIN 263 301 3 X APPROXIMATE REPEATS.
 FT REPEAT 263 273 2-1.
 FT REPEAT 277 287 2-2.
 FT REPEAT 291 301 2-3.
 FT DOMAIN 366 411 ASP/GLU/LYS-RICH.
 FT DISULFID 141 167 BY SIMILARITY.

RN [1]
RP SEQUENCE FROM N.A.


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CRTC_CABEL          STANDARD;          PRT;    395 AA.
ID  CRTC_CABEL
AC  P27798;
DT  01-AUG-1992 (Rel. 23, Created)
DT  01-AUG-1992 (Rel. 23, Last sequence update)
DT  28-FEB-2003 (Rel. 41, Last annotation update)
DE  Calreticulin precursor.
GN  CRR-1 OR Y38A10A.5.
OS  Caenorhabditis elegans.
OC  Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC  Rhabditidae; Peloderinae; Caenorhabditis.
OX  NCBI_TaxID=6239;
[1]
RN  SEQUENCE FROM N.A.
RP  STRAIN=Bristol N2;
RC  MEDLINE=92329978; PubMed=167827;
RX  Smith M.J.;
RT  "A C. elegans gene encodes a protein homologous to mammalian
RT  calreticulin."
RL  DNA Seq. 2:235-240 (1992).
[2]
RN  SEQUENCE FROM N.A.
RP  STRAIN=Bristol N2;
RC  Bauer C., Courtney L., Laplant Y.;
RL  Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
[3]
RN  REVISIONS.
RP  Waterston R.;
RL  Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC  -!- FUNCTION: This protein binds calcium. There are both high and low
CC  affinity calcium-binding sites.
CC  -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC  -!- SIMILARITY: Belongs to the calreticulin family.
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; X59589; CAA42159.1; -.
DR  EMBL; AF125963; AAD14746.1; -.
DR  PIR; S25851; S25851.
DR  WormPep; Y38A10A.5; CE21562.
DR  InterPro; IPR009033; Calret_calmex_P.
DR  InterPro; IPR001580; Calreticulin.
DR  InterPro; IPR008985; ConA_like Lec-gl.
DR  InterPro; IPR000886; ER_target_S.
DR  Pfam; PF00262; calreticulin; 1.
DR  PIRSF; PIRSF002356; Calreticulin; 1.
DR  PRINTS; PR00626; CALRETICULIN.
DR  ProDom; PD001866; Calreticulin; 1.
DR  PROSITE; PS00014; ER_TARGET; 1.
DR  PROSITE; PS00803; CALRETICULIN 1; 1.
DR  PROSITE; PS00804; CALRETICULIN 2; 1.
DR  PROSITE; PS00805; CALRETICULIN REPEAT; 3.
KW  Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
FT  SIGNAL          1 15
FT  CHAIN           16 395
FT  DOMAIN          193 301
FT  DOMAIN          302 395
FT  DOMAIN          186 250
FT  REPEAT          186 197
FT  REPEAT          205 216
FT  REPEAT          222 233
FT  REPEAT          239 250
FT  REPEAT          254 292
FT  REPEAT          254 264
FT  REPEAT          268 278
FT  REPEAT          282 292

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FT  DOMAIN          332 390
FT  DISULFID        133 158
FT  SITE            392 395
SQ  SEQUENCE        395 AA; 45616 MW; 35CA7D2EC1D56B03 CRC64;
Query Match          66.2%; Score 210.5; DB 1; Length 395;
Best Local Similarity 66.7%; Pred. No. 1.9e-18;
Matches 40; Conservative 7; Mismatches 12; Indels 1; Gaps 1;
QY  1 GPGTKKHVIFNYKGNVLINKDICKDDFFTHLYTLIVRPDNTYEVKIDNSQVESGSL 60
Db  134 GP-TRRVHVLNYKGNKLKKEITCKSDBLTHLYTLILNSDNTYEVKIDGSAQTGSL 192
RESULT 12
CRTC_CHLRE
ID  CRTC_CHLRE      STANDARD;          PRT;    420 AA.
AC  Q9STU3;
DT  16-OCT-2001 (Rel. 40, Created)
DT  16-OCT-2001 (Rel. 40, Last sequence update)
DT  16-OCT-2001 (Rel. 40, Last annotation update)
DE  Calreticulin precursor.
OS  Chlamydomonas reinhardtii.
OC  Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC  Chlamydomonadaceae; Chlamydomonas.
OX  NCBI_TaxID=3055;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=137c / CC-125;
RA  Zuppin A., Kaydanov C.;
RT  "Cloning and characterization of a cDNA encoding Chlamydomonas
RT  reinhardtii calreticulin."
RL  Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
CC  -!- FUNCTION: This protein binds calcium. There are both high and low
CC  affinity calcium-binding sites (By similarity).
CC  -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen (By similarity).
CC  -!- SIMILARITY: Belongs to the calreticulin family.
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC  -----
DR  EMBL; AJ000765; CAB54526.1; -.
DR  InterPro; IPR009033; Calret_calmex_P.
DR  InterPro; IPR001580; Calreticulin.
DR  InterPro; IPR008985; ConA_like Lec-gl.
DR  InterPro; IPR000886; ER_target_S.
DR  Pfam; PF00262; calreticulin; 1.
DR  PIRSF; PIRSF002356; Calreticulin; 1.
DR  PRINTS; PR00626; CALRETICULIN.
DR  ProDom; PD001866; Calreticulin; 1.
DR  PROSITE; PS00014; ER_TARGET; 1.
DR  PROSITE; PS00803; CALRETICULIN 1; 1.
DR  PROSITE; PS00804; CALRETICULIN 2; 1.
DR  PROSITE; PS00805; CALRETICULIN REPEAT; 1.
KW  Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
FT  SIGNAL          1 18
FT  CHAIN           19 420
FT  SITE            417 420
SQ  SEQUENCE        420 AA; 47327 MW; DD1BAJAF6F61C9B CRC64;
Query Match          62.6%; Score 199; DB 1; Length 420;
Best Local Similarity 61.0%; Pred. No. 5.2e-17;
Matches 36; Conservative 10; Mismatches 13; Indels 0; Gaps 0;
QY  1 GPGTKKHVIFNYKGNVLINKDICKDDFFTHLYTLIVRPDNTYEVKIDNSQVESGSL 59
Db  141 GYSTRKHVILTYKGNVLIKKDKAETDQUTHVTLVIKPDNTYQVLIDLKEVASGSL 199

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RESULT 13
CRTC PRUAR
ID CRTC BETVU STANDARD; PRT; 416 AA.
AC O81919;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Calreticulin precursor.
OS Beta vulgaris (Sugar beet).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;
OC Caryophyllales; Amaranthaceae; Beta.
OX NCBI_TaxID=161934;
RN SEQUENCE FROM N.A.
RP STRAIN=VV-D/ZRS; TISSUE=Leaf;
RC Viereck R.;
RA "Nucleotide sequence from sugar beet calreticulin."
RT Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
RL -!- FUNCTION: This protein binds calcium. There are both high and low
CC affinity calcium-binding sites (By similarity).
CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen (By similarity).
CC -!- SIMILARITY: Belongs to the calreticulin family.
CC
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CC
CC EMBL; AF134733; AAD32207.1;
DR InterPro; IPR009033; Calret_calmex_P.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR008985; ConA like lec_gl.
DR InterPro; IPR000886; ER target_S_g1.
DR Pfam; PF00262; calreticulin; 1.
DR PIRSF; PIRSF002356; Calreticulin; 1.
DR PRINTS; PR00626; Calreticulin.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00014; ER_TARGET; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 2.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal; Glycoprotein.
FT SIGNAL 1 25
FT CHAIN 26 416
FT CARBOHYD 57 57
FT CARBOHYD 157 157
FT SITE 413 416
FT SITE 416 416
SQ SEQUENCE 416 AA; 48136 MW; 565FEC3489F77CA7 CRC64;

Query Match 57.9%; Score 184; DB 1; Length 416;
Best Local Similarity 55.9%; Pred. No. 3.7e-15;
Matches 33; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

Dy 144 GYSTKKNVHAIYNNDTHNLKDKVCEFDQTHVTFILRPDAYSILIDNKEQKQSGSL 202

RESULT 14
CRTC PRUAR
ID CRTC PRUAR STANDARD; PRT; 421 AA.
AC O9X598;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Calreticulin precursor.
OS Prunus armeniaca (Apricot).

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OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
OX NCBI_TaxID=36596;
RN SEQUENCE FROM N.A.
RP STRAIN=cv. Bergeron; TISSUE=Endocarp, and Mesocarp;
RA Muegelle-A-Mbeugie D.; Nils-Lycaon B.R.;
RT "Molecular cloning and nucleotide sequence of a calreticulin from
RT apricot (Prunus armeniaca cv. Bergeron)".
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: This protein binds calcium. There are both high and low
CC affinity calcium-binding sites (By similarity).
CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen (By similarity).
CC -!- SIMILARITY: Belongs to the calreticulin family.
CC
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CC
CC EMBL; AF134733; AAD32207.1;
DR InterPro; IPR009033; Calret_calmex_P.
DR InterPro; IPR001580; Calreticulin.
DR InterPro; IPR008985; ConA like lec_gl.
DR InterPro; IPR000886; ER target_S_g1.
DR Pfam; PF00262; calreticulin; 1.
DR PIRSF; PIRSF002356; Calreticulin; 1.
DR PRINTS; PR00626; Calreticulin.
DR ProDom; PD001866; Calreticulin; 1.
DR PROSITE; PS00014; ER_TARGET; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 2.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal; Glycoprotein.
FT SIGNAL 1 22
FT CHAIN 23 421
FT CARBOHYD 56 56
FT CARBOHYD 156 156
FT SITE 418 421
FT SITE 421 421
SQ SEQUENCE 421 AA; 48416 MW; 4P5F94CBAA6C6690 CRC64;

Query Match 56.3%; Score 179; DB 1; Length 421;
Best Local Similarity 54.2%; Pred. No. 1.5e-14;
Matches 32; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

Qy 1 GPGTKKHVIFNYKGNVINKDKDEPHLYTLVIRPDNTYEVKIDNSQVESGSL 59
Dy 143 GYSTKKNVHAIYNNDTHNLKDKVCEFDQTHVTFILRPDAYSILIDNKEQKQSGSL 201

RESULT 15
CRTC DICDI
ID CRTC DICDI STANDARD; PRT; 424 AA.
AC Q23858;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Calreticulin precursor.
GN CRTA.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.
OX NCBI_TaxID=44689;
RN SEQUENCE FROM N.A.
RP STRAIN=AX3;
RA Mueller-Taubenberger A.; Gerisch G.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: This protein binds calcium. There are both high and low
CC affinity calcium-binding sites (By similarity).

```

```
CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -!- SIMILARITY: Belongs to the calreticulin family.
CC -----
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CC -----
CC EMBL: U36937; AAB8719.1; -.
CC DictyBase: DDB0001623; cttA.
CC InterPro: IPR009033; Calret_calmex_P.
CC InterPro: IPR001580; Calreticulin_.
CC InterPro: IPR008985; CnA_like_rec_gl.
CC InterPro: IPR000886; ER_target_S.
CC Pfam: PF00262; calreticulin; 1.
CC PIRSF: PIRSF002356; Calreticulin; 1.
CC PRINTS: PR00626; CALRETICULIN.
CC PRODOM: PD001866; Calreticulin; 1.
CC PROSITE: PS00804; CALRETICULIN_2; 1.
CC PROSITE: PS00805; CALRETICULIN_REPEAT; 1.
CC PROSITE: PS00014; ER_TARGET; 1.
CC Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
KW Endoplasmic reticulum; Calcium-binding; Repeat; Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 424 CALRETICULIN.
FT DOMAIN 191 257 4 X 12 AA APPROXIMATE REPEATS.
FT REPEAT 191 202 1-1.
FT REPEAT 211 222 1-2.
FT REPEAT 227 238 1-3.
FT REPEAT 246 257 1-4.
FT DOMAIN 260 298 3 X 11 AA APPROXIMATE REPEATS.
FT REPEAT 260 270 2-1.
FT REPEAT 274 284 2-2.
FT REPEAT 288 298 2-3.
FT DISULFID 105 137 BY SIMILARITY.
FT SITE 421 424 PREVENT SECRETION FROM ER (POTENTIAL).
SQ SEQUENCE 424 AA; 48350 MW; BAF273694FB6FC37 CRC64;
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Query Match 55.8%; Score 177.5; DB 1; Length 424;
Best Local Similarity 51.6%; Pred. No. 2.4e-14;
Matches 33; Conservative 14; Mismatches 12; Indels 5; Gaps 2;

Qy 1 GP----GKKVHVIFNYKGRVNLINKDI-RCKDFFTHLYTLIVRPDNTYEVKIDNSQVE 55
Db 133 GPDVCGASKRVHVLNLYKGRVNLINKDI-RCKDFFTHLYTLIVRPDNTYEVKIDNSQVE 192

Qy 56 SGSL 59
Db 193 AGNL 196

Search completed: October 4, 2004, 13:04:02
Job time : 9.82353 secs

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